

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 15:20:30 ; Search time 2213 Seconds

(without alignments)
10297.785 Million cell updates/sec

Title: US-09-870-501-2

Perfect score: 1089

Sequence: 1 cttctagggtcgtccgcgat.....gaataaaaaaaaaaaaaa 1089

Scoring table: IDENTITY_NUC

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Maximum Match 100%

Listing first 45 summaries

GenBank:*

1: gb_ba:*

2: gb_hlg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_hlg_hum:*

31: em_hlg_inv:*

32: em_hlg_other:*

33: em_hlg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	1089	100.0	1089	8	AB063117	AB063117 Hordeum v
2	511	46.9	1167	8	AF159254	AF159254 Zantedesc
3	475.8	43.7	1239	8	GHU37060	U37060 Gossypium h
4	449.4	41.3	1238	8	AF139190	AF139190 Mesembrya
5	444.4	40.8	1133	8	AB070626	AB070626 Cucurbita
6	438.6	40.3	1177	8	ATU69138	U69138 Arabidopsis
7	437	40.1	1045	8	ATAPEXT	X88276 A.thaliana
8	437	40.1	1121	8	AY065143	AY065143 Arabidops
9	437	39.8	1138	8	ATAPX	X88003 A.thaliana
10	433.6	39.8	1129	6	AF442387	AF442387 Capsicum
11	303.6	27.9	1229	6	BD005724	BD005724 Sequence
12	303.6	27.9	1229	6	BD005724	BD005724 Materials
13	301.4	27.7	1138	8	AF411228	AF411228 Hordeum v
14	293.8	27.0	1042	8	ZMAPXG	Z24934 Z.mays apx
15	290.8	26.7	1012	8	AF159627	AF159627 Fragaria
16	290.8	26.7	1058	8	AB050724	AB050724 Oryza sat
17	290.8	26.7	1160	8	AB053297	AB053297 Oryza sat
18	290.2	26.6	1040	8	AF159628	AF159628 Fragaria
19	286	26.3	1040	8	NTU15933	U15933 Nicotiana t
20	285.4	26.2	1035	8	AF159633	AF159633 Fragaria
21	285.4	26.2	1040	8	AF039953	AF039953 Fragaria
22	285.4	26.2	1065	8	AF159632	AF159632 Fragaria
23	284.8	26.2	1108	8	AF378131	AF378131 Zantedesc
24	282.8	26.0	1044	8	AF022213	AF022213 Fragaria
25	282.8	26.0	1097	8	AF053474	AF053474 Zantedesc
26	282.4	25.9	1050	8	HVU6	AJ006358 Hordeum v
27	282.2	25.9	1035	8	AF159630	AF159630 Fragaria
28	282.2	25.9	1051	8	AF159631	AF159631 Fragaria
29	281.2	25.8	1030	8	AF159629	AF159629 Fragaria
30	280	25.7	983	8	D45423	D45423 Rice mRNA f
31	278.8	25.6	756	8	ATAPCYT	X98275 A.thaliana
32	278	25.5	1055	8	TOBTCP	DB5912 Nicotiana t
33	277	25.4	753	8	AB078600	AB078600 Brassica
34	274.2	25.2	1117	8	VU061379	U61379 Vigna ungu
35	272.2	25.0	753	8	AB078599	AB078599 Brassica
36	271.4	24.9	1095	8	MCU43561	U43561 Mesembryant
37	270.6	24.8	753	8	RSAPX	X78452 R.salivus (
38	269.4	24.7	1023	8	ATASCOR	X59600 A.thaliana
39	269.4	24.7	1059	8	AY039879	AY039879 Arabidops
40	269.4	24.7	1060	8	AY056395	AY056395 Arabidops
41	269.2	24.7	1069	8	D88649	D88649 Cucumis sat
42	267.8	24.6	1064	8	GMU56634	U56634 Glycine max
43	267.4	24.6	1069	8	SPICAP	L20864 Spinacia ol
44	267.4	24.6	1083	8	SPICAP	D5864 Spinacia ol
45	267.2	24.5	1054	8	PSAPXI	X62077 P.sativum A

ALIGNMENTS

RESULT 1

AB063117

LOCUS

DEFINITION

Hordeum vulgare HvAPX1 mRNA for peroxisome type ascorbate

ACCESSION

AB063117

VERSION

AB063117.1 GI:15080681

KEYWORDS

SOURCE

Hordeum vulgare (cultivar:Haruna-nijo) early growth stage cDNA to

ORGANISM

Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poolidae; Triticeae; Hordeum.

1 (bases 1 to 1089)

REFERENCE

Shi,W.M., Muramoto,Y., Ueda,A. and Takabe,T.

Cloning of peroxisomal ascorbate peroxidase gene from barley and

enhanced thermostolerance by overexpressing in Arabidopsis thaliana

Gene. 273 (1), 23-27 (2001)

JOURNAL

MEDLINE

21376122

REFERENCE

2 (bases 1 to 1089)

AUTHORS

Takabe,T.

TITLE

Direct Submission

JOURNAL

Submitted (12-JUN-2001) Tetsuko Takabe, Nagoya University, Graduate School of Bioagricultural Sciences, Furoo-chou, Chikusa-ku, Nagoya, Aichi 464-8601, Japan (E-mail: h44854@nuc.cc.nagoya-u.ac.jp, Tel:81-52-789-5209, Fax:81-52-789-5209)

FEATURES

source

1. 1089
Location/Qualifiers

/organism="Hordeum vulgare"
/cultivar="Haruna-nijo"
/db_xref="taxon:4513"
/clone_lib="barley leaf cDNA"
/dev_stage="early growth stage"
/country="Japan"

gene

CDS

/gene="HvAPX1"
19. .894
/codon_start=1
/product="peroxisome type ascorbate peroxidase"
/protein_id="BAB62533.1"
/db_xref="GI:15080682"

BASE COUNT 299 a 245 c 267 g 278 t
ORIGIN

Query Match

Best Local Similarity 100.0%; Score 1089; DB 8; Length 1089;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTAGAGGTGTCGCGCATGGCGGCTCGGTGTGTGACGCCAGTACTCGCCAGATC 60
DB 1 CTCTAGAGGTGTCGCGCATGGCGGCTCGGTGTGTGACGCCAGTACTCGCCAGATC 60
QY 61 GACAGGGGCGCGCGCTTCCGTCCTCATGCGCTCCAAAGGATGCGCCCATCATG 120
DB 61 GACAGGGGCGCGCGCTTCCGTCCTCATGCGCTCCAAAGGATGCGCCCATCATG 120
QY 121 CTCGCGCTCGCATGATGATGCTGGCACTATGATGTAACAACAAGAACTGGTGTGA 180
DB 121 CTCGCGCTCGCATGATGATGCTGGCACTATGATGTAACAACAAGAACTGGTGTGA 180
QY 181 AATGTTCAATTAGATAGAGAGAGATACACCATGTTTCAATGCTGGCTTAAAAAT 240
DB 181 AATGTTCAATTAGATAGAGAGAGATACACCATGTTTCAATGCTGGCTTAAAAAT 240
QY 241 GCTATTGATCTCTTGAAGCTTATTAACGGAAGATCCAAAGATTACATATGACAGCTT 300
DB 241 GCTATTGATCTCTTGAAGCTTATTAACGGAAGATCCAAAGATTACATATGACAGCTT 300
QY 301 CATGAGCTGCGGAGTGTGAGTGAAGTGAAGGCGGCTCAACGCTTGAGTTGATC 360
DB 301 CATGAGCTGCGGAGTGTGAGTGAAGTGAAGGCGGCTCAACGCTTGAGTTGATC 360
QY 361 CTTGGAAGACGTGATGCTGACGTTTGTCCCGTGAAGAACGCTTCTGATGCTAAGAA 420
DB 361 CTTGGAAGACGTGATGCTGACGTTTGTCCCGTGAAGAACGCTTCTGATGCTAAGAA 420
QY 421 GGTGACCCACATCTTAAGGACATCTTTATGCAATGGGTTTAAACAGACAAAGATTGTA 480
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QY 481 GCAATATCTGGGGGCGACAGCTGGGAAAGCGCATCTGAAAGTCTGGTTGACGCT 540
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QY 541 GCATGACTCTGACCTCTGAATTTGACAACTATCTTTCTTGAGCTACTGAAGGG 600
DB 541 GCATGACTCTGACCTCTGAATTTGACAACTATCTTTCTTGAGCTACTGAAGGG 600

QY 601 GAATCTGAGGGTCTCTGTAAGCTCCCTACTGATTAAGCAATGTTGGATGATCTGAAATTT 660
DB 601 GAATCTGAGGGTCTCTGTAAGCTCCCTACTGATTAAGCAATGTTGGATGATCTGAAATTT 660
QY 661 CGACGCTATGTGAGCTTTATGCAAGAGATGAGATGTTTCTTCAAGACTACGCTGAA 720
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QY 781 AATACAGATGTTTCAACTGCTGTTGATGTCACAGAGTGAAGTGGGTGACAGTGGCT 840
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QY 841 GGAGGCTGATGATGCGGGGCTACCTGATGACAGGCTTCCAAAGAGAGCAAGTAAGGGGT 900
DB 841 GGAGGCTGATGATGCGGGGCTACCTGATGACAGGCTTCCAAAGAGAGCAAGTAAGGGGT 900
QY 901 CGTGAATCTTGATGATGATGCTCTTATTTAGTATGATCAAGTATATTTAAAAAA 960
DB 901 CGTGAATCTTGATGATGATGCTCTTATTTAGTATGATCAAGTATATTTAAAAAA 960
QY 961 TAAGTCCCAAGTGCATAATACAGAACTGATGATGAACAACAAGTACTGCAAAAT 1020
DB 961 TAAGTCCCAAGTGCATAATACAGAACTGATGATGAACAACAAGTACTGCAAAAT 1020
QY 1021 ATTGATCATCTTCTGAGACATCTCTCTCATATATATACATCTGATGATTAATAA 1080
DB 1021 ATTGATCATCTTCTGAGACATCTCTCTCATATATATATACATCTGATGATTAATAA 1080
QY 1081 AAAAAAAAA 1089
DB 1081 AAAAAAAAA 1089

RESULT 2

AF159254

LOCUS AF159254 1167 bp mRNA linear PLN 07-MAY-2001
DEFINITION Zantedeschia aethiopica ascorbate peroxidase (cmprx) mRNA, complete cds

AF159254

AF159254.1 GI:5442409

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

/organism="Zantedeschia aethiopica"
/db_xref="taxon:59721"
/tissue_type="young leaf"
1. 1167
/gene="cmprx"
52. .918
/gene="cmprx"
/EC_number="1.11.1.11"
/note="putative glyoxysomal membrane-bound protein"
/product="ascorbate peroxidase"
/protein_id="AA043334.1"

REFERENCE
AUTHORS Lino-Neto, T., Tavares, R.M., Palme, K. and Pais, M.S.S.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Biology, University of Minho, Campus de Gualtar, Braga 4710, Portugal
FEATURES
source 1. 1167
/organism="Zantedeschia aethiopica"
/db_xref="taxon:59721"
/tissue_type="young leaf"
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/gene="cmprx"
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/gene="cmprx"
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/note="putative glyoxysomal membrane-bound protein"
/product="ascorbate peroxidase"
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/db_xref="GI:5442410"
/translation="MAAPVADGYLKEVDKARLDLIALKNCAPVMLRLAMDAGT
YDVAKTGGPNISIRNEEHRKAGNAKIDICEYVKAHPKRYTADLYOLAGVA
VEWNGPTIDEPGRDLSVPRKGRDLDAOGSAHLDVFRMGLSPKDIYALSGH
TLGRAHPERSGDPWMEPLKPDNSYVELLEGRBELTLIPDKYVDEPERGKY
ELRKADDEAFPRDIYAKSHKLSLELFTSPKASRSDAHTSILLASAVAVAAVVF
LSYCEVRSRK"

BASE COUNT 326 a 249 c 280 g 312 t
ORIGIN

Query Match 46.9%; Score 511; DB 8; Length 1167;
Best Local Similarity 75.0%; Pred. No. 7e-117;
Matches 656; Conservative 0; Mismatches 210; Indels 9; Gaps 1;

19 ATGGGGGCTCCGGTGTGGAGCCCGAGTACCTGCGCAGGTGGACAGGCGCGCCGCC 78
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Db 52 ATGGGGGCGCGGTGTGGAGCGGGCTACCTCAAGAGAGTGGACAGCGCGCGAGGAGC 111
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 79 TTCCGTCCTCATGCGCTCCAGAGGAGTGGCCCCCATCATGCTCCGCTCGCATGGCAT 138
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 112 CTCCCGCGCCCTCATGCGCAGCAAGAACTGCGCTCCGCTCATGCTCCGCTCATGCGCAT 171
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QY 139 GATGCTGGCACTATGATGTGAACAAGAACTGGTGGTCAAAATGGTCAATTTAGATAC 198
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 172 GATGCTGGCACTATGATGTGAACAAGAACTGGTGGTCAAAATGGTCAATTTAGATAC 231
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 199 GAGGAAGAGTACACCATGGTCAATGCTGGCTTAAATTTGCTATTTGATCTCTTGAG 258
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 232 GAGGAAGAGTACACCATGGTCAATGCTGGCTTAAATTTGCTATTTGATCTCTTGAG 291
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QY 259 CCTATTAAGCAAGCATCCAAAGATATATGCAAGACCTTCATCAGCTTGCGGAGTA 318
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Db 292 ACGGTGAAGCAAAACATCCAAAGATATATGCAAGACCTTCATCAGCTTGCGGAGTA 351
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QY 319 GTTGGAGTGAATACCGGGGGTCCAAACCGTGGTTCATCCCGGAGAGTATTCG 378
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Db 352 GTTGGAGTGAATACCGGGGGTCCAAACCGTGGTTCATCCCGGAGAGTATTCG 411
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QY 379 TCAAGTTTCCCGGAGAGGAGCCCTTCTGATGTGAAGAAGAGTGCACACATCTAAG 438
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Db 412 TTGGTTTCCCAAGAGAGGAGTCTGATGTGAAGAAGAGTCTGATCTAAG 471
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QY 439 GACATCTTTATTCGAATGGGTTAAACAGCAAAAGATATTTGACATCTATCTGGGGGCG 498
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Db 472 GATGTTTATTCGAATGGGTTAAACAGCAAAAGATATTTGACATCTATCTGGGGGCG 531
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QY 499 ACCGTGGGAGAGGCGATCTGAAAGGCTGGGTTGAGGTCGATGAGACTCGTACCT 558
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Db 532 ACATTTGGAGAGGCTCATCAGAGAGTCAAGCTTTGATGTCTTGGACAAATGAACCT 591
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QY 559 CTGAATTTGACACACTCATCTTCTTGAAGTACTGAAGGGGAAATCTGAGGGTCTTCTG 618
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Db 592 CTGAATTTGACACACTCATCTTCTTGAAGTACTGAAGGGGAAATCTGAGGGTCTTCTG 651
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QY 619 AAGCTCCTACTGATAGGCAATTTGATGATCTGAATTTGACAGCTTGAGAGCTT 678
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Db 652 AAGCTCCTACTGATAGGCAATTTGATGATCTGAATTTGACAGCTTGAGAGCTT 711
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QY 679 TATGCAAGGATAGGATTTTCTTCAAGGACTACGCGATTCACACAAAAGCTTCT 738
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Db 712 TTTGCTAGAGATAGGATTTTCTTCAAGGACTACGCGATTCACACAAAAGCTTCT 771
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QY 739 GAATCTGGCTTCACACAGAGAGTGGCCAGCATCTACAAAATTCAGATTTTCAAT 798
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Db 772 GAATCTGGCTTCACACAGAGAGTGGCCAGCATCTACAAAATTCAGATTTTCAAT 822
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QY 799 GCTGTGTACTTTCACAGAGTCAAGTCCGGGTAGCAAGTGTGACAGCTGTATTCGG 858
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Db 823 ACCACTACTTATAGCTCAGAGCGCTGTGGAGTGTGCTGCTGCTGTGTCTCTTA 882
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QY 859 GGCTACCTGTAGAGCTTCCAAAGAGAGCAAGTA 893
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Db 883 ACTTACTGCTATGAAGTATCTAGAGAGCAAGTA 917
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RESULT 3
GH037060
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 1239)
Bunkelmann, J. R. and Trellease, R. N.
Ascorbate peroxidase. A prominent membrane protein in oilseed
glyoxysomes
910xysomes
Plant Physiol. 110 (2), 589-598 (1996)
MEDLINE
6351186
REFERENCE
2 (bases 1 to 1239)
Trellease, R. N.
Direct Submission
JOURNAL
Submitted (25-SEP-1995) R. N. Trellease, Botany, Arizona State
University, Tempe, AZ 85287-1601, USA
Location/Qualifiers
1..1239
/organism="Gossypium hirsutum"
/cultivar="Deltapine 62"
/db_xref="taxon:3635"
94..960
/note="glyoxysomal membrane-bound protein"
/product="ascorbate peroxidase"
/protein_id="AAB52954.1"
/db_xref="GI:1019946"
/translation="MAAPVADGYLKEVDKARLDLIALKNCAPVMLRLAMDAGT
YDVAKTGGPNISIRNEEHRKAGNAKIDICEYVKAHPKRYTADLYOLAGVA
VEWNGPTIDEPGRDLSVPRKGRDLDAOGSAHLDVFRMGLSPKDIYALSGH
TLGRAHPERSGDPWMEPLKPDNSYVELLEGRBELTLIPDKYVDEPERGKY
ELRKADDEAFPRDIYAKSHKLSLELFTSPKASRSDAHTSILLASAVAVAAVVF
LSYCEVRSRK"

polyA_signal
BASE COUNT 346 a 262 c 287 g 344 t
ORIGIN

Query Match 43.7%; Score 475.8; DB 8; Length 1239;
Best Local Similarity 72.1%; Pred. No. 4.4e-108;
Matches 637; Conservative 0; Mismatches 237; Indels 9; Gaps 1;

12 GTCCGGATGGCGGCTCCGGTGGTGGAGCCCGAGTACCTGCGCAGGTGGACAGGCGCG 71
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Db 87 GACTTCAATTCGGCTTCCAGTACGTATACCGAGTATCTCAAGAGATGATTAAGCTTG 146
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QY 72 CCGCGCTTCCGTGCCCTCATGCTCCAAAGGATGGCCCCCATCATGCTCGCCTCGC 131
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Db 147 TCGAGACCTTCGCGCTCATGCGCTTGAAGAAATTCGCTCATCATGCTCGCTTACG 206
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QY 132 ATGGCATGTGCTGGCAGCTATGATGTGAACACAGAACTGTGGTGGCAATGGTCAAT 191
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Db 207 GTGGACGATGTGGGACATGATGTGACACTAAACCGGAGGTCCAAATGGCTCTAT 266
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QY 192 TAGATACGAGGAAGATACACCATGGTTCATATGCTGTGCTTAAATTTGCTATTGATCT 251
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Db 267 AAGGAATGAAGAGATTACATCATGCGCCCAATAGCGCTTGAAATTCGCTATTGATTT 326
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QY 252 CCTGAGCCTATTAAGCAAGACATCCAAAGATTATATGCAAGACCTTCATCAGCTTGC 311
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Db 327 TTGTGAGGAAGTGAAGGCTTAACATCTTAATTTAGCTATGCAAGACCTTATACAGCTTGC 386
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QY 312 CCGAGTAGTTCAGATTGAAGTCAAGCGGGGTCCCAACCGTTGATGATTCATCTCGGAAGACG 371
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Db 387 TGTGTGTGTTGTTGAAGTCACTGAGAGTCTCTACATTTGATGCTGGAAGAA 446
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Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
OY	372	TEAATCGTAGATTTGTCCTCCCGTGAAGACAGCCCTCCGTAATGCTAAAGAAAGGTGACACACA	AF139190	1238 bp	mRNA	linear	PLN 16-MAY-1999				
Db	447	GGATTCATAACATTGTGCCCCAGGGAAGCCGACTTCCAGATGCTMAAAGAGGTGCACCTTA	AF139190								
OY	432	TCTAAGGACATCTTTTATTCGAATGGGGTTTAAACAGACAAAGATATTGTAGCACTATCGG	AF139190								
Db	507	TCGTGAGAGACATCTTCATTCGTAATGGGTCTTTCTGACAAAGATATTGTGGCATTTATCTGG	AF139190								
OY	492	GGGGGACACACCTGGGGAAGGGCATCCTAAAGGTGTGGGTTTGAACGTGACATGACCTCG	AF139190								
Db	567	GGGTACACACTCTGGGAAGGGCTTCATCTAGAGATCAGGTTTTGTATGGTGGCCCTTGGACCA	AF139190								
OY	552	TGACCCCTCTGAATTTGACAACTCATCTCTTTCTTGAAGTCTGAAGGGGGAATCTGACGG	AF139190								
Db	627	TGAAOCCCTGAAAGTTGACAACTCTTACTTCTGAGAGTGTAAAGGGGAATCTGAAG	AF139190								
OY	612	TCTTCTGAAGCTCCCTCAGATATGAGGCATTTGTGATGATCTGAATTTGACAGCTTANGT	AF139190								
Db	687	GCTTTTGAACATCTCCAAACAGACAGGCTTTGTATGATGACCCGTGATGCCGAAGATATGT	AF139190								
OY	672	GGAGCTTTATGCAAAAGATGAGGATTTCTTCTTCAAGAGCTACCGGTATGCACACAAAA	AF139190								
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	HTLGGABERSGSGP	PTOEDLKFNDNS	VFLLGSEGLLOLP	DTDAALVEDPFRERY
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Query Match	41.3%	Score 449.4;	DB 8;	Length 1238;
Best Local Similarity	70.1%;	Pred. No. 1.7e-101;		
Matches 625; Conservative	0;	Mismatches 251;	Indels 15;	Gaps 1

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Db	105	TCATCAATGGCAGTGGCACCGGTGGTGCACAGTGTACTCTCAAGAAATGCACAGGCT	166
OY	70	CGCCGCGCCTTCGGTCCCTCATCGCTCCACAGGGATGCGCCCCCATCATGCTCGCCTC	123
Db	165	CGTGGCAGTCTTTCGACACATCTCTTAATGCGAGCTCGCTCTCTTCAATGCTCGCCTC	224
OY	130	GCATGGCATATGCTGGACCGCTATGATATGACCAAGAACTGGTGGTCAATGGTCTCA	185
Db	225	GCCTGGCAGACGCTGGACGTAATGTCTCGAAGACGAAACCGGGTGGCGCTAATGGCTCC	288
OY	190	ATTAGATACAGAGAAAGATACACCATTGGTTCAAATCGCTTAAATTTGCTATTCAT	249
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Db	405	GTCTGTGTCTTTCATTTAATGACCTGAGAGCGGCACATTAATTTTCTCTGTATGA	466
OY	370	CGTGATTCGTAGTTTGTCCCGGTGAAGAGACGCTTCTGATGCTTAAGAAAGTGCACCA	425
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OY	490	GAGGGGACACGCGTGGAAAGGCGCATCTGAAAGGCTGTGGTTGACGGTGCATGAGACT	549
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VERSION	U69138.1	GI:2444018		
KEYWORDS				
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ORGANISM	thale cress. Arabidopsis thaliana			
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AUTHORS	Zhang,H., Wang,J., Nickel,U., Allen,R.D. and Goodman,H.M.			
TITLE	Cloning and expression of an Arabidopsis gene encoding a putative peroxisomal ascorbate peroxidase			
JOURNAL	Plant Mol. Biol. 34 (6), 967-971 (1997)			
COMMENT	2 (bases 1 to 1177) Zhang,H., Wang,J., Nickel,U., Allen,R.D. and Goodman,H.M. Direct Submission Submitted (03-SEP-1996) Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409, USA On Sep 30, 1997 this sequence version replaced gi:2435396. Location/Qualifiers			
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Matches 612; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

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 VERSION AY065143.1 GI:17473760
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 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
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 1 (bases 1 to 1121)
 REFERENCE
 AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pflam,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shimizu,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Submitted (03-DEC-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,

USA
 e-mail for correspondence: arab@sequence.stanford.edu
 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pflam,P.K., Sakano,H., Shimizu,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
 Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.
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 Best Local Similarity 69.6%; Pred. No. 2,1e-98;
 Matches 612; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

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DEFINITION X98003
ACCESSION X98003.1 GI:1332438
VERSION APX gene; ascorbate peroxidase.
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SOURCE
ORGANISM Arabidopsis thaliana
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AUTHORS Jespersen, H.M.
TITLE Direct Submision
JOURNAL Submitted (21-MAY-1996) H.M. Jespersen, University of Copenhagen,
Department of Protein Chemistry, Oester Farimagsgade 2A, DK-1353
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2 (bases 1 to 1127)
REFERENCE Jespersen, H.M., Kjaergaard, I.V., Ostergaard, L. and Welinder, K.G.
AUTHORS From sequence analysis of three novel ascorbate peroxidases from
TITLE Arabidopsis thaliana to structure, function and evolution of seven
JOURNAL types of ascorbate peroxidase
MEDLINE Biochem. J. 326 (Pt 2), 305-310 (1997)
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BASE COUNT 323 a 245 c 273 g 286 t
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Query Match 40.1%; Score 437; DB 8; Length 1127;
Best Local Similarity 69.6%; Pred. No. 2,1e-98;
Matches 612; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

QY 16 GCCATGGCGGCTCCGGTGTGGACGCGGAGTACTGCGCCAGGTGACAGGCGCGCGC 75
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DEFINITION AF442387
ACCESSION AF442387
VERSION AF442387.1 GI:17066704
KEYWORDS
SOURCE Capsicum annum.
ORGANISM Capsicum annum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 1138)
Hwang, B.K. and Do, H.M.
Pepper ascorbate peroxidase and thiolredoxin peroxidase genes
regulate H2O2 accumulation and peroxidase activity during the
bacteria-induced hypersensitive reaction in Capsicum annum
Unpublished
2 (bases 1 to 1138)
Hwang, B.K. and Do, H.M.
Direct Submission
Submitted (02-NOV-2001) College of Life and Environmental Science,
Molecular Plant Pathology Laboratory, Korea University, Anam-dong,
Sungbuk-gu, Seoul 136-701, Republic of Korea
FEATURES
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/note="CAPOA1"
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CDS
BASE COUNT 354 a 213 c 261 g 310 t
ORIGIN

Query Match 39.8%; Score 433.6; DB 8; Length 1138;
Best Local Similarity 69.0%; Pred. No. 1.5e-97;
Matches 614; Conservative 0; Mismatches 264; Indels 12; Gaps 1;

QY 13 FCCGCGATGGCGGCTCCGGTGTGACGCGGAGTACCTGCGGCGAGTGACAGGGCGCGC 72
DB 18 TCTCCATGGCGAAGCAATGTGCTACTGATACATCAAGAATGAGAAAGCTCGT 77
QY 73 CCGGCTTCCGTGCTCATTCGCTCCAGAGGATGGCGCCCATCATGTCCGCCCTCGCA 132
DB 78 CCGGACCTCCGGCTCTCTCCACAAAACCTGCTCTATCAWGGCTTCGCTTAGCA 137
QY 133 TGGCATGATGCTGGACACTATGATGACACAGAACTGTGGTGCATATGTTCAATT 192
DB 138 TGGCAGATGACGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 197
QY 193 AGATACGAGGAAGATACACCAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTT 252
DB 198 AGAAATGAGGAAGATACCTACCTACCTGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTT 257
QY 253 CTGACGCTTAAATGAGGATGACCAAGATTAATGATGATGATGATGATGATGATGATGATG 312
DB 258 TGTGAGCAGTGAATGTCACAAAGATTAATGATGATGATGATGATGATGATGATGATGATG 317

QY 313 GGATGATGTCAGTGAAGTCAACCGGGGGTCCACACCGTTGAGTTCATCCCTGGAAGACGT 372
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QY 373 GATTCGTCAGTTTGTCCCGGTGAGAGCGCTTCTGATGCTAAGAGGTGACCACT 432
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DB 558 GAGCCCTGAAATTTGACATTCATTTTGTGAGCTCTTAAAGGGGAAAGTGAAGGC 617
QY 613 CTTCGAGCTCCCTACATGATGATGATGATGATGATGATGATGATGATGATGATG 672
DB 618 CTACTGAAACTACCCACAGACATGCTTATGATGATGATGATGATGATGATGATGATG 677
QY 673 GAGCTTTATGAAAGGATGAGATGTTTCTTCAAGACTGATGATGATGATGATGATG 732
DB 678 GAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 737
QY 733 CTTCGAACTGTGCTTCAACACCGAGGACGATGATGATGATGATGATGATGATGATG 792
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QY 793 TCACTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 852
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QY 853 ATCCGCGGCTACCTGACGACGATGATGATGATGATGATGATGATGATGATGATG 902
DB 846 GACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 895

RESULT 11
AR074176 1229 bp DNA linear PAT 28-AUG-2000
LOCUS AR074176
DEFINITION Sequence 85 from patent US 5952486.
ACCESSION AR074176
VERSION AR074176.1 GI:10000936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1229)
AUTHORS Bloksberg, L.N., Havukkala, I. and Grierson, A.W.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 5952486-A 85 14-SEP-1999;
FEATURES
source
1..1229
/organism="unknown"
BASE COUNT 342 a 256 c 292 g 339 t
ORIGIN

Query Match 27.9%; Score 303.6; DB 6; Length 1229;
Best Local Similarity 63.4%; Pred. No. 4.5e-65;
Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

QY 16 GCGATGCGGCTCCGGTGTGACGCGGAGTACCTGCGGAGTGCACAGGCGCGCCGC 75
DB 222 GTGAAGGCTTATCCCAAGGAGAGTACCAAGGCTGCCATTGACAAATGCAAGAGG 281
QY 76 GCTTCGCTGCTCATTCGCTCCCAAGGATGCGCCCATCATGATGCTCGCTCGATG 135
DB 282 AAGCTCCGAGCTCTCATTCAGAGAAAGACTGTGCGCCCATCATGATGCTTCCATG 341

QY	136	CATGATGCGGACCGACCTATGATGTGAACACAGAAGACCTGGGATGGCAAAATGGTTCATATTA	195
Db	342	CACACCGCTGGGACCTTACGATGTGCTCAAGACCAAGACCAGGAGCCCTTGGGACGATGACA	401
QY	196	TACGAGGAAGATACACCCATGCTTCAATGCTGGCTTTAAAAATTGCTATTAATCTCTT	255
Db	402	TATGGGCGGACCTTGCCACAGGTGTGTACAGTAGGTGTGGACATGCAATTAGGCTCCGG	461
QY	256	GAGCCTATTAAAGCGAAGCATCCAAAGATTACATATGACAGACCTTCATGACTTGGCGGA	315
Db	462	GAGCCAAATCAAGGAACAGTTCCCATTAACACCTATGCTGACCTTTATCATGTTGGCTGAT	521
QY	316	GTATGTGACGTTGAAGTGCACCGGGGGTCCAAACGGTTGAGTTATCCCTGGGAAGAGTGAT	375
Db	522	GTGGTGGCTGTTTGAAGTGAACCGGGGACCTGACATTTCCGTTCAATCTTGAAAGAGAGAC	581
QY	376	TCGTGACGTTTGTCCCGGTGAGAGAGCGCTTCTCTGATGCTAAGAAAGGTGCACCACATCTA	435
Db	582	AAGCCTGAGACCTCCAGAAGAAAGCGCGCTTCTCTGATGCTAAGAAAGGACCTGATCATCTG	641
QY	436	AGGGACATCTTTTATTCGAATGGGGGTTTAACAGACAAAGATATTGTAGCACTATCTGGGGG	495
Db	642	AGGGATGTTTTTGGTCAATGGGGTTGATGATTAAGAAATGTGGCCCTGTCTGGTGGCC	701
QY	496	CACACCTGGGAAAGCGCATCTCTAAAGAGTCTGGGTTTGACGGTGACATGACCTGGTGC	555
Db	702	CACACCTTGGGAGATGCGCACAGAGAGATCTGGTTTGAAGGACATAGGACCTCTAAC	761
QY	556	CCTCTGAATTTGACACCTCATCTTTCTTGTAGCTACTGAAGAGGGGAAATCTGAGGGTCTT	615
Db	762	CCCTTATCTTTTGAACACTCTTACTTCAAGAGCTGTGGATCTGAGAGAGAAAGGAGCCCT	821
QY	616	CTGAAGCTCCGACATGAAGAAGCATTTGGATGATGATCCGAATTTTCAGACGCTATGTGGAG	675
Db	822	CTTCAATGCGATCTGATGAAGGACACTGCTGCTGATCTCTAGTTTTCAGATTATGTGTAG	881
QY	676	CTTATGCAAGAGATGAGAGATTTTCTTCAAGAGCTACGCTGAATCAACAAAAAATCT	735
Db	882	AAGTATGCACAGAGAGAGACGACTTCTTCTGTGACTATGCGGAAGCTCAGCTGAAGCTT	941
QY	736	TCTGACTTGGCTT 749	
Db	942	TCTGAATTTGGGTT 955	
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LOCUS	BD005724	1229 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Materials and methods for the modification of plant lignin content.		
ACCESSION	BD005724		
VERSION	BD005724.1	GI:18634095	
SOURCE	JP 2001500378-A/85.		
ORGANISM	unidentified.		
REFERENCE	unclassified.		
AUTHORS	1 (bases 1 to 1229)		
TITLE	Bloksberg, L.N., Grierson, A.W. and Havukkala, I.J.		
JOURNAL	Materials and methods for the modification of plant lignin content		
	Patent: JP 2001500378-A 85 16-JAN-2001.		
	GENESTS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS		
COMMENT	LTD		
	OS Unidentified		
	PN JP 2001500378-A/85		
	PD 16-JAN-2001		
	PF 10-SEP-1997 JP 1998513535		
	PR 11-SEP-1996 US 08/771000		
	PI LEONARD NATHAN BLOKSBERG, ALISTAIR WALLACE GRIERSON, PI ILKKA		
	JAAKKO HAVUKKALA		
	PC C12N15/53, C12N15/54, C12N15/52, C12N15/60, C12N15/82, A01H5/00 CC		
	Strandedness: Single;		
	CC Topology: Linear;		
	FH Key Location/Qualifiers		

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source			Location/Qualifiers	
			1..1229	
BASE COUNT	342 a	256 c	292 g	339 t
ORIGIN				
Query Match	27.9%	Score 303.6;	DB 6;	Length 1229;
Best Local Similarity	63.4%	Pred. No. 4.5e-65;		
Matches 463;	Conservative	0;	Mismatches 269;	Indels 0;
				Gaps 0
16	GCAGTGGCGGCTCCGGTGTGTGACGCGCGATGCTCCGCCAGTGTGACAGAGGCGCGCGC	75		
Db	222 GTGAAGCTTATCCACACCGTAACCGAGAGTACAAAGGCTGCCATTGACAAATGCAAGG	281		
QY	76 GCCTCCGTCCTCATCGCTTCCAAAGGATCGCCGCCCATATGCTCGCTCGATGG	135		
Db	282 AAGCTCCGACCTCTCATTTGCGAAGAACTGTGGCGCATCATGTTGCAATGCAATG	341		
QY	136 CATGATCTGGACACCTATGATGTGAAACACAAACATGGTGGGCAAAATGCTCAATAGA	195		
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QY	196 TACGAGGAGAGTACACCCATGGTTCAAATGCTGGCTTTAAAAATGCTATTGATCTCTT	255		
Db	402 TATGGGCGCCAGCTTCACGCTCCCGATGCTTACAGTGTGTGACATCGCATGGATGGCTCG	461		
QY	256 GAGGCTATTAAAGCAAGCATCCAAAGATTAAATATGACAGACCTTCATCAGCTTGCCGGA	315		
Db	462 GAGCATATCAAGAACAGTTCGCCCATATACCACTTATGCTGACCTTTTCACTGGCTGGT	521		
QY	316 GTATGTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT	375		
Db	522 GTGTCGCTGTGAAGTGAACCGGGGACCTGACATTCGCTTCATCCTGGAGAGAGAGAC	581		
QY	376 TCGTCACTTTGTCCTCCGTGAAGAGCGCTTCTGATGCTTAAGAAAGGTGCACCATCTA	435		
Db	582 AAGGCTGAGGCTCCAGAAAGGCGGCTTCCTGATGCTTACAAAGGACCTGATCATCTG	641		
QY	436 AGGACATCTTTTATGATGGGGTTTAAAGCAAAAGATTTGTAGCAATATGTCATGCGGGG	495		
Db	642 AGGATATTTTGTGTACATGAGGTTGAATGTATTAAGAAATTTGGCTTGTCTGGTGGC	701		
QY	496 CACAGCTGGGAAAGGCGCATCTCTGAAAGCTTGGGTTTGAACGCTGATGAGCTCTGAC	555		
Db	702 CACACCTTGGGAGATGACCAAGAGAGATGTGTTTGAAGACCATGACCTGTAAAC	761		
QY	556 CCGTGAATTTGACAACTATCTTCTTGTAGCTACGTAAGAGGGGAAATGTGAGGCTT	615		
Db	762 CCGCTTATCTTACAACTCTTACTTTCACAGGCTTGTGACTGGAAGAAAGGCGCTG	821		
QY	616 CTGAAGCTCCCTACTATTAAGCATTTGTGTGATGATCTCTGAAATTTCCACGCTATGTGAG	675		
Db	822 CTTCAGTTGCACTGTATTAAGCACTGCTGTGCTACTTCTTGTGCTACTATGCGAAGCTC	881		
QY	676 CTTTATGCAAGAGATGAGATGTTTCTTCAAGGACTACGCTGATATACCAAAAATCTT	735		
Db	882 AAGTATGCAAG	941		
QY	736 TCTGACTGGCTT 749			
Db	942 TCTGAACTGGCTT 955			
RESULT 13				
LOCUS	AF411228	1138 bp	mrna	linear
DEFINITION	Hordium vulgare ascorbate peroxidase mRNA, complete cds.			
ACCESSION	AF411228			
VERSION	AF411228.1	GI:15808778		
KEYWORDS				

SOURCE	ORGANISM	barley.
REFERENCE	AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Poales; Poaceae;
TITLE	JOURNAL	Pooled; Triticeae; Hordeum.
ADTHORS	JOURNAL	1 (bases 1 to 1138)
TITLE	JOURNAL	Dunford,R.P. and Laurie,D.A.
JOURNAL	JOURNAL	Unpublished
REFERENCE	JOURNAL	2 (bases 1 to 1138)
ADTHORS	JOURNAL	Dunford,R.P. and Laurie,D.A.
TITLE	JOURNAL	Direct Submission
JOURNAL	JOURNAL	Submitted (17-AUG-2001) Crop Genetics, John Innes Center, Colney Lane, Norwich, Norfolk NR4 7UH, UK
FEATURES	source	Location/Qualifiers 1..1138 /organism="Hordeum vulgare" /cullivar="Morex" /db_xref="taxon:4513" /note="derived from EST with GenBank Accession Number BF254073" 78..848 /codon_start=1 /product="ascorbate peroxidase" /protein_id="AAI08496.1" /db_xref="GI:15808779" /translation="MAAKCYPTVSDEYLAAYAKARRKRLRGLIAEKNCAPILMLRIAMHSAGFVAVTKGPGPIGMKCPALAHGNANAGDIALVRLEPITSEDFOLAGVVAVEVGEPVEVPHPRODKPEPPPELADIDOGSDHLEKOVSTOMLSDDOIVALSGGTLTQRCHREKSGFEFGAATNPLIDNSFTLLSGERKGLQLPDVKYLTPDPAREPLVDXKAEDDAEFADYAEAKHLKSIFREASEGGC"
BASE COUNT	ORIGIN	218 a 347 c 322 g 251 t
Query Match	Best Local Similarity	27.7%; Score 301.4; DB 8; Length 1138; Matches 477; Conservative 0; Mismatches 271; Indels 3; Gaps 1;
QY	3	TCCTAGGCTCCCGCATGCGCGCTCCGGTGCGGACGCCAGTACTCGCCGAGTGC
DB	71	TCCAGCCATGCGCCGCAAGTGTCTACCACAAGGTTGACGACGATCTGCGCGCTGC
QY	63	CAGGCGCGCGCGCTTCCGTGCTTATGCTTCCGAAGGATCGCCCATCATCT
DB	131	CAGGCGCGCGCGCAAGCTCCGTGGCTTATGCGCCAGAAGAACCTCGCGCCCTCATCT
QY	123	CCGCTCCATGCGCATGATGCTGGCACCTATGATGTGAACAACAAGCTGGGTGCAAA
DB	191	CCGCTCCGCTGGGCACTGCGCGCGGACCTTGCACGTGGCCACCAAGACCGGCGGCTT
QY	183	TGCTTCAATTAGATACGAGAAAGTACACCCATGTTCAATGCTGGCTTAATAATTC
DB	251	CGGCAACATGAAGTGGCCCCGGGAGCTGCGCCAGGCGGCCCAAGCGCGGCTCGACATGC
QY	243	TATGATCTCTTGAACCTATTAAAGCAAGCATCCAAGATTCATATATGACACCTTCA
DB	311	CGTAGGCTGCTCGACGCCATCAAGGACACATCCCTCCCTCTCTACGCGGCACTTCTA
QY	303	TCAGCTTCCGAGAGTGTGACATTGAAGTACCGGGGGTCCACACCGCTGATTCATGCC
DB	371	CCAGCTCGCTGGAGTCTGCGCGCTCGAGGTACCGGCGGCTGAGGTTCCCTTCACACC
QY	363	TGGAAGACGTATTCGTGATTTGTCCTCCGTAAGGAGACGCTTCCTGATGCTGAAGAAG
DB	431	CGGAGACAGGACAAAGCCGAGAGCTCTCCGAGAGGCGCTTCTCTGATGCGCACCCAAAG
QY	423	TGCACACATCTTAAGGACATCTTT--ATCGAATGGGGTTAACAGACAAAGATATTGT
DB	491	CTTCGACACCTTCAGGCGAGGTGTTTCCACATCAGATGGGTGATGACACAGACATGCT
QY	480	AGCACTATCTGGGGGGGACACGCGGGAAGAGCGCATCTCAAAGCTGGGTGATGACGG
DB	551	TGCTCTTTCTGTGGTCCACCTCTGGGAAGATGCCACAAGAGAGATCTGGGGTTGAAGG

QY	540	TGCAGCTGCTGACCTCTGAAATTTGACAACTCATCTTCTTGAGCTACTGAAGG	599
Db	611	AGCCGAGACCGCAACCCCTTTCATCTTCGACAACTCTTACTTCACTGAGCTCTCTAGTGG	670
QY	600	GGATCTGAGGGCTCTTCTGAAAGCTCCCTACTGATGAAGCATTGTTGGATGATCTGAAAT	659
Db	671	GGAGAAAGAAAGGTCTTCTTCAAGTTCGCCGACGAAAGGCTGCTGACTGACCCGGCCTT	730
QY	660	TCGAGCGTATGTGGAGCTTTATGCAAGAGTATGAGATGTTTCTTCAGAGCTACGCTCA	719
Db	731	CGGCCACTTGTGGCAAAATATGCTGCGGATGAGGATGCTGCTTCTTGCTGACTAGCCGA	790
QY	720	ATCACACAAAACCTTCTGAACTGGGCTTC	750
Db	791	GGCACACCTCAAGCTCTCTGAACTTGAGATTTC	821
RESULT 14			
ZMAPXG	LOCUS	ZMAPXG	1042 bp mRNA linear PLN 01-DEC-1999
DEFINITION		2.mays apx gene encoding cytosolic ascorbate peroxidase.	
ACCESSION		Z34934	
VERSION		Z34934.1	GI:600115
KEYWORDS		cytosolic ascorbate peroxidase.	
SOURCE		Zea mays.	
ORGANISM		Zea mays	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	
AUTHORS		Van Breusegem, F., Villarroel, R., Van Montagu, M. and Inze, D.	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 1042)	
AUTHORS		Van Breusegem, F.	
TITLE		Direct Submission	
JOURNAL		Submitted (04-JUL-1994) Van Breusegem F., Labo voor Genetika, Universiteit Gent, Ledeganckstraat 35, Gent, Belgium, 9000	
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Matches 467; Conservative 0; Mismatches 267; Indels 3; Gaps 1;			
QY	16	GGGATGGCGGCTCCGGTGTGGAGCCGAGTACCTGCGCCGAGTGTGAAGGCGCGCCG	75
Db	75	GTGAAGGCTTACCCACGAGTGAAGGAGTCAAGGCGGCTGACAGCCCAAGCT	134

76 GCCTTCCTGCTCCATCCGCTCCAAAGGATGCGCCGCCCATCATGCTCCGCTCCGATG 135
135 AAGCTCCGGGGCTCATCGCCGAGAAATGCGCCGCTCATGCTCCGCTCCGATG 194
136 CATGATGCTGCACCTATGATGTGAACACAAGAACTGGTGGCAATGGTCAATAGA 195
195 CACTCGGTGGGCACTTCATGTGTGTCACCAAAACCGGGGGCCCTTGGCACCATAG 254
196 TACGAGAAAGATACACCCATGATGATGATGCTGCTTAAATTTGCTATGATCTCT 255
255 AACCCCGTGGAGAGCGCGACGGTCCAAACCGGAGCTGAAATGGCATACAGCTCTGA 314
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316 GTAGTTGACGTTGAACTGACCGGGGGTCCAAACGTTGAGTTCACTCCCTGGAAAGCTGAT 375
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435 AAGCTGAGCTTCACCGGAAAGCGCTTCTGATGCTACCAAGGTTCTGAACCTC 494
436 AAGGACATCTTTT--ATGAATGGGGTTAACAAGACAAGATATGTAGACTATCTGGG 492
495 AAGCAGGTTTCTCCACACAGATGGTGTGAAGGACGAGACATGTTGGCTTTCTGGT 554
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613 CTTCGAAGCTCCCTACATATAAGCATCTGTGATGATCTCAATTTGACACCTATGTC 672
675 CTTCGACACTACCAAGTACCAAGCCCTCTCTCTGATTCATCTCCGCCCACTGTT 734
673 GAGCTTTATGAAGAGATGAGTGTCTTCTTCAGAGACTACGCTGAATACACAATAAA 732
735 GACAAATACGACGAGGAGGAGGAGCTTCTTGTGCTGACTACGCCAGGCCACCTGAAG 794
733 CTTCGTAAGCTTGGCTT 749
795 CTTCGAAATTTGGGAT 811

RESULT 15
AF159627 1012 bp mRNA linear PLN 16-NOV-2001
LOCUS AF159627
DEFINITION Fragaria x ananassa cytosolic ascorbate peroxidase (APX) mRNA,
APX18 allele, complete cds.
ACCESSION AF159627
VERSION AF159627.1 GI:5257545
KEYWORDS
SOURCE
ORGANISM
Fragaria x ananassa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Rosoidae; Fragaria.
REFERENCE
AUTHORS Kim,I.J., Lee,B.H., Jo,J. and Chung,W.I.
TITLE Sequence variability of nine cytosolic ascorbate peroxidases in
polyploid strawberry
JOURNAL DNA Seq. 11 (6), 475-484 (2001)
MEDLINE 21554286
PUBMED 11696974
REFERENCE 2 (bases 1 to 1012)
AUTHORS Kim,I.J. and Chung,W.I.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Biological Sciences, Korea Advanced

Institute of Science and Technology, 373-1 Kusong-dong, Yuseong-gu,
Taejeon 305-701, Korea
Location/Qualifiers
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/note="Fragaria x ananassa Duch."
1. 1012
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BASE COUNT 233 a 241 c 252 g 286 t
ORIGIN
Query Match 26.7%; Score 290.8; DB 8; Length 1012;
Best Local Similarity 62.8%; Pred No. 6.8e-62;
Matches 485; Conservative 0; Mismatches 282; Indels 5; Gaps 2;
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QY 94 GCCTCAAGGATGCCGCCCATCATGCTCCGCTGCGATGCGATGATGCTGGCACTAT 153
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QY 214 CATGTTCAAAATGCTGCTTAAATTTGCTATGATCTCTTGAAGCTATTAACGGAAG 273
Db 246 CACGGCGCTTAACAATGCTCTGACATTTGCTGACGCTGCTGAGCCGATCAAGAGCA 305
QY 274 CATCCAAAGATTACATATGACAGCTTCAAGCTTCCCGGAGTGGTGAATTAATC 333
Db 306 TTCCCTATTTCTCTTACGCTGACTTACCAAGTGGGAGTGTGCTGCTGAGGTC 365
QY 334 ACCGGGGTCCAAACGTTGATCATCTCCGTAAGACGATGCTGATGTTGCCCGT 393
Db 366 ACCGGTGAACCTGATGTTCCATTTCCACCGAAGAGAGAAACCCAGACCAACA 425
QY 394 GAAGAACGCTTCTGATGCTTAAGAAAGGTGACACCATCTAAGGAGACATCTT--TAT 450
Db 426 GAAGCGCTTCTTCTGATGCTGAAAGGTTCTGACCACTTGAAGGAAAGTGTGGCAA 485
QY 451 CGAATGGGTTAACAGCAAAATATTTAGACATCTTGGGGGACACACCTGGGAAG 510
Db 486 ACCATGGGTCTACGACACGACATGTTGCTCTCTGCTGAGTGTGACACCTTGGGAAG 545
QY 511 GCGCATCTGAAGAGCTGGGTTTACGAGTGCATGATGATGATGATGATGATGATGATG 570
Db 546 GCGCAACAAGAAAGCTGATTTGAAGGACCATGATGATGATGATGATGATGATGATG 605
QY 571 AACTCATCTTCTTGAAGTACTGAAGGGGAATCTGAAGGCTTCTGAAGTCTCTACT 630
Db 606 AACTCATATTTCACTGTCTATTTAGTGAAGAAAGGCTTCTGAAGTCTCTACT 665
QY 631 GATTAAGCATTTGTTGATGATCTGAAATTTGCAAGCTTATGATGAGCAATGAAGAT 690

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 31 Seconds

(without alignments)
1623.920 Million cell updates/sec

Title: US-09-870-501-1

Perfect score: 1498
Sequence: 1 MAAPVDAEYLROYDRARRA.....AVAAAVIAGYLYEASKRSK 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mmc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1498	100.0	291	10	0941C3 hordeum vul
2	1240.5	82.8	288	10	039780 gossypium h
3	1205.5	80.5	288	10	09XGS8 zantedesch
4	1189.5	79.4	286	10	0948P1 cucurbita s
5	1183	79.0	287	10	042564 arabidopsi
6	1152	76.9	287	10	081810 arabidopsi
7	1135.5	75.8	287	10	09XFC0 mesembryant
8	934.5	62.4	279	10	065634 arabidopsi
9	836.5	55.8	250	10	040589 nicotiana t
10	834.5	55.7	250	10	039843 glycine max
11	832.5	55.6	250	10	042941 nicotiana t
12	828	55.3	256	10	0945R5 hordeum vul
13	827.5	55.2	250	10	09SMD3 lycopersico
14	824.5	55.0	250	10	041772 zea mays (m
15	824	55.0	249	10	096399 cucumis sat
16	823.5	55.0	250	10	042661 capsicum an

17	821.5	54.8	250	10	P93404 oryza sativ
18	821.5	54.8	250	10	Q41712 vigna ungu
19	820.5	54.8	250	10	09SYW5 glycine max
20	820.5	54.8	250	10	093XM9 zantedesch
21	819.5	54.7	249	10	042459 spinacia ol
22	819.5	54.7	250	10	049159 fragaria an
23	818.5	54.6	250	10	09S7F7 fragaria an
24	818.5	54.6	250	10	09S7F5 fragaria an
25	818.5	54.6	250	10	065161 fragaria an
26	817.5	54.6	250	10	09S7F6 fragaria an
27	817.5	54.6	250	10	048919 fragaria an
28	816.5	54.5	250	10	023983 hordeum vul
29	816.5	54.5	250	10	Q43758 glycine max
30	816	54.5	246	10	09SFC9 arabidopsi
31	815.5	54.4	250	10	043824 arabidopsi
32	815	54.4	251	10	039006 arabidopsi
33	809.5	54.0	251	10	09FED1 oryza sativ
34	799.5	53.4	250	10	09SED0 pimlinella
35	789.5	52.7	250	10	P93657 brassica na
36	784.5	52.4	250	10	Q94CF7 suada mari
37	775.5	51.8	260	10	042909 mesembryant
38	774.5	51.7	245	10	081603 mesembryant
39	752.5	50.2	250	10	049122 brassica ju
40	746.5	49.8	254	10	081604 mesembryant
41	714.5	47.7	309	10	Q41371 spinacia ol
42	674	45.0	189	10	09FPE1 pinus strob
43	666	44.5	415	8	046921 spinacia ol
44	656.5	43.8	386	8	09CNL9 nicotiana t
45	656.5	43.8	435	8	Q9XPR6 nicotiana t

ALIGNMENTS

RESULT 1	ID	Q941C3	PRELIMINARY:	PRT:	291 AA.
AC	Q941C3:				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	PEROXISOME TYPE ASCORBATE PEROXIDASE.				
GN	HVAPX1.				
OS	Hordeum vulgare (Barley).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC	Triticeae; Hordeum.				
OX	NCBI_TaxID=4513;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. HARUNA-NIJO:				
RX	MEDLINE=21376122; PubMed=11483357;				
RA	Shi W.M., Muramoto Y., Ueda A., Takabe T.;				
RT	"Cloning of peroxisomal ascorbate peroxidase gene from barley and				
RT	enhanced thermostolerance by overexpressing in Arabidopsis thaliana."				
RL	EMBL: AB063117; BAB62533.1; .				
DR	EMBL: AB063117; BAB62533.1; .				
KW	Peroxiidase. 291 AA; 31708 MW; 707A5C7D53AA524D CRC64;				
SQ	SEQUENCE				
Query Match	100.0%; Score 1498; DB 10; Length 291;				
Best Local Similarity	100.0%; Pred. No. 4.4e-115;				
Matches	291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 MAAPVDAEYLROYDRARRAFALIASKGCADIMRLAMHDAGTYDVNTRGGANGSIRY 60				
DB	1 MAAPVDAEYLROYDRARRAFALIASKGCAPIMRLAMHDAGTYDVNTRGGANGSIRY 60				
QY	61 EEEYHGSNAGIKIADIDLEPIKAKHKPTTYADHQLAGVAVETGCPVTEFICGRDS 120				
DB	61 EEEYHGSNAGIKIADIDLEPIKAKHKPTTYADHQLAGVAVETGCPVTEFICGRDS 120				
QY	121 SWCPREGRLPAKKGAPHLRDIFFYRMGLTDKDIVALSGHSIGKAKHPERSGFDGAWTRDP 180				

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Db 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
QY 181 LKFDSNYFLELLKGSEGLKLTPTDKALLDDPEFRRYVELYAKDEDFEFNDYESHKRLS 240
Db 181 LKFDSNYFLELLKGSEGLKLTPTDKALLDDPEFRRYVELYAKDEDFEFNDYESHKRLS 240
QY 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLYEASKRSK 291
Db 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLYEASKRSK 291

RESULT 2
ID Q39780 PRELIMINARY; PRT; 288 AA.
AC Q39780;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ASCORBATE PEROXIDASE.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DELTAPINE 62;
RX MEDLINE=96351186; PubMed=8742335;
RA Bunkelman J.R., Trelease R.N.;
RT "Ascorbate peroxidase. A prominent membrane protein in oilseed
RT glyoxysomes.";
RL Plant Physiol. 110:589-598(1996).
DR EMBL: U37060; AAB52954.1; -.
DR HSSP: P48534; IAPX.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase.1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
DR KX Peroxidase.
SQ SEQUENCE 288 AA; 31942 MW; ADP15C705ED54C4E CRC64;

Query Match 82.8%; Score 1240.5; DB 10; Length 288;
Best Local Similarity 80.4%; Pred. No. 6.1e-94;
Matches 234; Conservative 26; Mismatches 28; Indels 3; Gaps 1;

Db 1 MAAPVDAEYLROVDRARAFRLIASKGAPIMLRAMHMDAGTYDVNTRTGANGSIRY 60
QY 1 MAAPVDAEYLROVDRARAFRLIASKGAPIMLRAMHMDAGTYDVNTRTGANGSIRY 60
Db 1 MAFPVVDTEYLKEIDKARDLRLILKNCAPIMLRAMHMDAGTYDVSTKGGPNSIRN 60
QY 61 EEEYTHGNSAGLKIAIDLEPIKAKHPKITTYADLHQLAGVAVAVETGGPTVEPIGRSDS 120
Db 61 EEEYTHGNSAGLKIAIDLEPIKAKHPKITTYADLHQLAGVAVAVETGGPTIDVPGKSDS 120
QY 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
Db 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
QY 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
Db 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
QY 181 LKFDSNYFLELLKGSEGLKLTPTDKALLDDPEFRRYVELYAKDEDFEFNDYESHKRLS 240
Db 181 LKFDSNYFLELLKGSEGLKLTPTDKALLDDPEFRRYVELYAKDEDFEFNDYESHKRLS 240
QY 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLYEASKRSK 291
Db 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLYEASKRSK 291

RESULT 3
ID Q9XGS8 PRELIMINARY; PRT; 288 AA.
AC Q9XGS8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)

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DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ASCORBATE PEROXIDASE (EC 1.11.1.11).
GN CMAPX.
OS Zantedeschia aethiopica (White calla lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Zantedeschia.
OX NCBI_TaxID=69721;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Lino-Neto T., Tavares R.M., Palme K., Pais M.S.S.;
RT "Expression of ascorbate peroxidase during senescence and regreening
RT of Zantedeschia aethiopica spathe.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF159254; AAD43334.1; -.
DR HSSP: P48534; IAPX.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase.1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
DR KX Peroxidase; Oxidoreductase.
SQ SEQUENCE 288 AA; 31433 MW; 28BBBCFELL1CBFD63 CRC64;

Query Match 80.5%; Score 1205.5; DB 10; Length 288;
Best Local Similarity 78.0%; Pred. No. 4.6e-91;
Matches 227; Conservative 33; Mismatches 28; Indels 3; Gaps 1;

QY 1 MAAPVDAEYLROVDRARAFRLIASKGAPIMLRAMHMDAGTYDVNTRTGANGSIRY 60
Db 1 MAAPVDAEYLROVDRARAFRLIASKGAPIMLRAMHMDAGTYDVNTRTGANGSIRY 60
QY 61 EEEYTHGNSAGLKIAIDLEPIKAKHPKITTYADLHQLAGVAVAVETGGPTVEPIGRSDS 120
Db 61 EEEYTHGNSAGLKIAIDLEPIKAKHPKITTYADLHQLAGVAVAVETGGPTIDVPGKSDS 120
QY 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
Db 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
QY 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
Db 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERKSGFGAMTRDP 180
QY 181 LKFDSNYFLELLKGSEGLKLTPTDKALLDDPEFRRYVELYAKDEDFEFNDYESHKRLS 240
Db 181 LKFDSNYFLELLKGSEGLKLTPTDKALLDDPEFRRYVELYAKDEDFEFNDYESHKRLS 240
QY 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLYEASKRSK 291
Db 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLYEASKRSK 291

RESULT 4
ID Q948P1 PRELIMINARY; PRT; 286 AA.
AC Q948P1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PEROXISOMAL ASCORBATE PEROXIDASE.
GN Cucurbita sp. cv. Kurokawa Amakuri.
OS Cucurbita sp. cv. Kurokawa Amakuri.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=170542;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KUROKAWA AMAKURI;
RX MEDLINE=21109356; PubMed=11158440;
RA Nito K., Yamaguchi K., Kondo M., Hayashi M., Nishimura M.;
RT "Pumpkin peroxisomal ascorbate peroxidase is localized on peroxisomal
RT membranes and unknown membranous structures.";
RL Plant Cell Physiol. 42:20-27(2001).
DR EMBL: AB070626; BAB64351.1; -.

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KM Peroxidase. 286 AA; 31562 MW; 48C6EC7997F012C0 CRC64;
 SQ SEQUENCE
 Query Match 79.4%; Score 1189.5; DB 10; Length 286;
 Best Local Similarity 77.3%; Pred. No. 9.4e-90;
 Matches 225; Conservative 28; Mismatches 33; Indels 5; Gaps 1;
 QY 1 MAPVDAEYLROVDARRARAFALIASKGCAPIMRLAMWHDAGTYDVNTRTGANGSTRY 60
 DB 1 MALPVDAEYLKEIKARRELRLALIANRNCAPIMRLAMWHDAGTYDVNTRTGANGSTRY 60
 QY 61 EEEYHGSNAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPGTFEIPGRDS 120
 DB 61 EEEYHGSNAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPGTFEIPGRDS 120
 QY 121 SVPCEGRPLDPAKKAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPERSGFDGAWTRDP 180
 DB 121 RSPBGRPLDPAKKAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPERSGFDGAWTRDP 180
 QY 181 LKFDNSYFLEILKGSEGLIKLPTDKALIDDEPRFRYVELYAKDDEVPFKDYAESHKILS 240
 DB 181 LKFDNSYFLEILKGSEGLIKLPTDKALIDDEPRFRYVELYAKDDEVPFKDYAESHKILS 240
 QY 241 ELGFPNRSRGPASTKSDYSTAVVLAOSAGVAAVYAGLYEASRSK 291
 DB 241 ELGFPNRSRGPASTKSDYSTAVVLAOSAGVAAVYAGLYEASRSK 291
 RESULT 5
 ID 042564 PRELIMINARY; PRT; 287 AA.
 AC 042564;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ASCORBATE PEROXIDASE (EC 1.11.1.11) (L-ASCORBATE PEROXIDASE).
 GN APX OR APX3 OR MEX13.60 OR ATG63500.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucots II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLOMBIA;
 RA Jespersen H.M., Kirsgaard I.V.H., Ostergaard L., Melinder K.G.;
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Karpinski S., Escobar C., Karpinski B., Creissen G., Mullineaux P.;
 RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97435981; Pubmed=9290648;
 RA Zhang H., Wang J., Nickel U., Allen R.D., Goodman H.M.;
 RT Cloning and expression of an Arabidopsis gene encoding a putative
 RT peroxisomal ascorbate peroxidase.";
 RL Plant Mol. Biol. 34:967-971(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Zhang H., Wang J., Nickel U., Allen R.D., Goodman H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Purnelle B., Boutry M., Goffeau A., Hohlsel J., Mewes H.W.,
 RA Mayer K., Schueller C.; to the EMBL/GenBank/DBJ databases.
 RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.

RA Purnelle B., Boutry M., Goffeau A., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- CATALYTIC ACTIVITY: L-ASCORBATE + H(2)O(2) = DEHYDROASCORBATE + 2
 CC H(2)O.
 DR EMBL; U69138; AAB71493.1; -;
 DR EMBL; X98003; CA66640.1; -;
 DR EMBL; X98276; CA66926.1; -;
 DR EMBL; AL022023; CA17765.1; -;
 DR EMBL; AL161586; CAB80217.1; -;
 DR HSSP; P48534; IAPX.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF00141; peroxidase.1.
 DR PRINTS; PR00458; PEROXIDASE.1.
 DR PROSITE; PS00435; PEROXIDASE_1; 1.
 DR PROSITE; PS00436; PEROXIDASE_2; 1.
 KW Peroxidase; Oxidoreductase.
 SQ SEQUENCE 287 AA; 31572 MW; B348E74BA34115DE CRC64;
 Query Match 79.0%; Score 1183; DB 10; Length 287;
 Best Local Similarity 75.9%; Pred. No. 3.2e-89;
 Matches 221; Conservative 34; Mismatches 32; Indels 4; Gaps 1;
 QY 1 MAPVDAEYLROVDARRARAFALIASKGCAPIMRLAMWHDAGTYDVNTRTGANGSTRY 60
 DB 1 MAPVDAEYLKEIKARRELRLALIANRNCAPIMRLAMWHDAGTYDQASKTGPGNGSTRN 60
 QY 61 EEEYHGSNAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPGTFEIPGRDS 120
 DB 61 EEEYHGSNAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPGTFEIPGRDS 120
 QY 121 SVPCEGRPLDPAKKAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPERSGFDGAWTRDP 180
 DB 121 SVPCEGRPLDPAKKAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPERSGFDGAWTRDP 180
 QY 121 NVCPEGRPLDPAKKAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPERSGFDGAWTRDP 180
 DB 121 NVCPEGRPLDPAKKAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPERSGFDGAWTRDP 180
 QY 181 LKFDNSYFLEILKGSEGLIKLPTDKALIDDEPRFRYVELYAKDDEVPFKDYAESHKILS 240
 DB 181 LKFDNSYFLEILKGSEGLIKLPTDKALIDDEPRFRYVELYAKDDEVPFKDYAESHKILS 240
 QY 241 ELGFPNRSRGPASTKSDYSTAVVLAOSAGVAAVYAGLYEASRSK 291
 DB 241 ELGFPNRSRGPASTKSDYSTAVVLAOSAGVAAVYAGLYEASRSK 291
 RESULT 6
 ID 081810 PRELIMINARY; PRT; 287 AA.
 AC 081810;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ASCORBATE PEROXIDASE.
 GN APXIII.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucots II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLOMBIA;
 RA Escobar C., Bradley D.J., Puente P., Harberd N., Creissen G.P.,
 RA Mullineaux P.M.;
 RT "Ascorbate peroxidase III gene from Arabidopsis thaliana is regulated
 RT by light and development.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ006030; CAA06823.1; -;
 DR HSSP; P48534; IAPX.
 DR InterPro; IPR002016; Peroxidase.

DR PFAM PF00141; PEROXIDASE_1.
DR PRINTS; PR00458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KW Peroxidase.
SQ SEQUENCE 287 AA; 31585 MW; 05BC1E228FA0B4 CRC64

OY		66	HGSNAGLKAIADLLEPIRAKHKITYADIHLQLAGVAAVEVTGGPVIETPGCRDSSVCBR	125
Db		65	RPHNGKEAFAAFCEEVAKHPHRSVAYDLXOLAGVAAVEVGGPAIIPFTGPKRDKADSAD-	123
OY		126	BGRLDARDAKGAPHLRIDFIYRMGLTJTKDILVALSGSHSLCKAPHERSGPFGCAWTRDDLPKPN	185
Db		124	DGEFLPNEGASHLTLSLRMGLEDRDDIVALLSGGHTTLGRAHKERKDEFECPWTQDPPLKFDN	183
OY		186	SYLELLLGEGSELKLKTPTDRALDDOPEFRRYVELYARDEDVFYFODYESHKKLSLSELT	245
Db		184	SYFELLTGEPFGILLQTKTDKRALDDPPKFPVPVKLYANDEDMFFAAYAISHHKLSELGN	243
OY		246	PRSSSPASTKDVSATVAVLAQSASVAAAANYINGLYEASKRK	291
Db		244	PPRRIPSA-----VTQOTIGIAAAAAVVIFTICYEASRRKK	279
<hr/>				
RESULT 9				
ID	Q40589	PRELIMITARY;	PR:	250 AA.
AC	Q40589;			
DT	01-NOV-1996	(TREMBLrel_01, Created)		
RT	01-NOV-1996	(TREMBLrel_01, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel_19, last annotation update)		
DE	CYSOSOLIC ASCORBATE PEROXIDASE.			
OS	Nicotiana tabacum (common tobacco).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
NCBI_TaxId=4097;	Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Shigeoka S., Ishikawa T.;			
RL	"cDNA encoding a cytosolic ascorbate peroxidase from tobacco."			
Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; D85912; BAAL2918.1; -.			
DR	HSSP; P48534; LAPX.			
DR	InterPro: IPRO02016; Peroxidase.			
DR	Pfam; PF00141; peroxidase; 1.			
DR	PRINTS; PR00458; PEROXIDASE.			
DR	PROSITE; PS00435; PEROXIDASE_1; 1.			
DR	PROSITE; PS00436; PEROXIDASE_2; 1.			
KW	Peroxidase.			
SO	SEQUENCE	250 AA;	27450 MM;	7A7926564C05A07 CRC64;
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Query Match 55.8%; Score 836.5; DB 10; Length 250;				
Best Local Similarity 66.1% Pred. No. 7.6e-61;				
Matches 160; Conservative 28; Mismatches 53; Indels 1; Gaps 1;				
OY		4	FVYAEEYLROYDRBARAFRALIASGCAPIMLRLAMHDAGTYDVNTFRIGANGSTIREBE	63
Db		6	PYVSEELIKAYDKCKRKIRGLIAENKCNPMLMKRLAMHSAGITDYSCSKTGGPBGVIKRFAYE	65
OY		64	YTHGSMAGLIKAIADLLEPIKAHKHPIITYAADLHQLAGVAAVEVTGGPYTEFTIGRRDSSVC	123
Db		66	QGHNAGNIDIALRIELPERIKEQPILTSGDEPYQLAGVAAVEVTGGPDVPFHNGREDKTER	125
OY		124	PREGRLPARAKGAHPLRDIFXR-WGLTKDIYALSOGSHSLGKAHERSGCFDCAMTRDPLK	182
Db		126	PVERRLPATGTGSDHLRVFVKOMGLSKDIDLVALSGGHTLTRCHKERSGFBGPMTTNPLI	185
OY		183	FDNSYFELLEKGESGILLKPTDRALDDOPEFRRYVELYARDEDVFYFODYESHKKLSL	242
Db		186	FDNSYFELLEKGESGILLQTPSRKALLSDPAFRPLYEKTADEDAEFADYAEAHKLISEL	245
OY		243	GF	244
Db		246	GF	247

[illegible]

DT 01-DEC-2001 (TREMBLE rel. 19, last annotation update)
DE CYTOSOLIC ASCORBATE PEROXIDASE.
GN APX.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H99;
RA Van Breusegem F., Villarroel R., Van Montagu M., Inze D.;
RT "Ascorbate peroxidase cDNA from maize.";
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: Z34934; CAAB4406.1; -
DR HSSP; P48534; IAPX.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
KW Peroxidase
SO SEQUENCE 250 AA; 27312 MW; D5B6AB7BFF9E6A86 CRC64;

Query Match	55.0%	Score 824.5	DB 10	Length 250
Best Local Similarity	64.8%	Pred. No. 7.3e-60		
Matches 158; Conservative	33;	Mismatches 52;	Indels 1;	Gaps 1;

[illegible]

RESULT 15

ID	096399	PRELIMINARY;	PRT;	249	AA.
AC	096399:				
DT	01-FEB-1997	(TIREMBLrel. 02, Created)			
DT	01-FEB-1997	(TIREMBLrel. 02, Last sequence update)			
DT	01-DEC-2001	(TIREMBLrel. 19, Last annotation update)			
DE	CYTOSOLIC ASCORBATE PEROXIDASE.				
OS	Cucumis sativus (Cucumber).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid1; Cucurbitales; Cucurbitaceae; Cucumis.				
OX	NCHI_Taxid-3659;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=SEEDLINGS;				
RA	Amako K., Sano S., Miyake C., Cao W., Asada K.;				
RT	cDNA cloning of cytosolic ascorbate peroxidase from cucumber and its				
RT	overexpression in Escherichia coli.				
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.				
DR	HMSL; D88649; BA13671.1; -				
DR	HSSP; P48534; IAPX				
DR	InterPro; IPR002016; Peroxidase.				
DR	Pfam; PF00141; peroxidase.1.				
DR	PRINTS; PR00458; PEROXIDASE.				

DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KW Peroxidase.
SQ SEQUENCE 249 AA; 27395 MW; 8C41BAF5EE9657F CRC64;

Query Match	55.0%	Score 824	DB 10	Length 249
Best Local Similarity	64.3%	Pred. No. 8e-60		
Matches 155	Conservative 32	Mismatches 54	Indels 0	Gaps 0

[illegible]

Search completed: October 23, 2002, 13:57:21
Job time : 34 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 32 Seconds
(without alignments)
1010.077 Million cell updates/sec

Title: US-09-870-501-1
Perfect score: 1498
Sequence: 1 MAAPVDAEXLRQVDARRA.....AFAAAVVIAGLYEASRKRK 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1183	79.0	287	21	Arabidopsis thaliana
2	1183	79.0	287	21	Arabidopsis thaliana
3	1152	76.9	287	21	Arabidopsis thaliana
4	1061	70.8	254	21	Arabidopsis thaliana
5	1061	70.8	254	21	Arabidopsis thaliana
6	818.5	54.6	250	21	Arabidopsis thaliana
7	818.5	54.6	250	21	Arabidopsis thaliana
8	818.5	54.6	250	21	Arabidopsis thaliana
9	818.5	54.6	250	21	Arabidopsis thaliana
10	818.5	54.6	250	21	Arabidopsis thaliana
11	818.5	54.6	250	21	Arabidopsis thaliana

12	818.5	54.6	250	21	Arabidopsis thaliana
13	818.5	54.6	254	21	Arabidopsis thaliana
14	818.5	54.6	297	21	Arabidopsis thaliana
15	818.5	54.6	297	21	Arabidopsis thaliana
16	737.5	49.2	215	21	Arabidopsis thaliana
17	737.5	49.2	215	21	Arabidopsis thaliana
18	737.5	49.2	215	21	Arabidopsis thaliana
19	737.5	49.2	215	21	Arabidopsis thaliana
20	737.5	49.2	215	21	Arabidopsis thaliana
21	737.5	49.2	215	21	Arabidopsis thaliana
22	737.5	49.2	215	21	Arabidopsis thaliana
23	650.5	43.4	191	21	Arabidopsis thaliana
24	650.5	43.4	191	21	Arabidopsis thaliana
25	650.5	43.4	191	21	Arabidopsis thaliana
26	650.5	43.4	191	21	Arabidopsis thaliana
27	640.5	42.8	354	21	Arabidopsis thaliana
28	640.5	42.8	426	21	Arabidopsis thaliana
29	640.5	42.8	452	21	Arabidopsis thaliana
30	631.5	42.2	348	21	Arabidopsis thaliana
31	631.5	42.2	348	21	Arabidopsis thaliana
32	631.5	42.2	353	21	Arabidopsis thaliana
33	631.5	42.2	372	21	Arabidopsis thaliana
34	629.5	42.0	347	21	Arabidopsis thaliana
35	629.5	42.0	353	21	Arabidopsis thaliana
36	484	32.3	122	17	Arabidopsis thaliana
37	477.5	31.9	182	21	Arabidopsis thaliana
38	405	27.0	136	21	Arabidopsis thaliana
39	405	27.0	140	21	Arabidopsis thaliana
40	405	27.0	164	21	Arabidopsis thaliana
41	405	27.0	164	21	Arabidopsis thaliana
42	377	25.0	238	21	Arabidopsis thaliana
43	374	25.0	102	21	Arabidopsis thaliana
44	373.5	24.9	266	21	Arabidopsis thaliana
45	373.5	24.9	339	21	Arabidopsis thaliana

ALIGNMENTS

RESULT 1
ID AAG09460 standard; Protein: 287 AA.
AC AAG09460;
DF 17-Oct-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7405.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0133240.
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PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.

XX 17-FEB-2000.
PD 04-AUG-1999; 99WO-EP05652.
XX 04-AUG-1998; 98EP-0202634.
PR 04-AUG-1998; 98EP-0202634.
XX
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX Lee JH, Verbruggen N;
PI WPI; 2000-205726/18.
XX N-PSDB; AA298313.
DR
PT Isolation of polynucleic acids useful for producing transgenic plant by
isolating genes involved in tolerance to environmental stress
PT
PS Claim 12; Page 112-115; 312pp; English.
XX
XX The invention relates to isolation of coding sequences and/or genes
involved in tolerance to environmental stress in plants. The sequences
CC (AA298305-298365) are useful for producing a transgenic plant having
enhanced tolerance or resistance to environmental stress conditions such
CC as anaerobic, flooding, cold, dehydration, drought, heat stress or
salinity. This is useful for producing improved yield, growth,
CC development and productivity under environmental stress conditions, and
also provides growth of crops in areas where they cannot grow without
the induced osmotolerance. Sequences AA27925-984 represent polypeptide
CC sequences from A. thaliana that are encoded by the genes involved in
environmental stress tolerance.
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SQ Sequence 287 AA;
Query Match 76.9%; Score 1152; DB 21; Length 287;
Best Local Similarity 75.0%; Pred. No. 2.4e-114;
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DB 1 MAAPVDAEYLKRETKARRELSLIANKNCAPIMLRMLAMHDAGTYDAQSKGPGRSIRN 60
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DB 61 EEEHTHGANSGLIKALDCEGVAKHPKITADLYQLAGVAVVEYTGPTDLYFVYGRKDS 120
QY 121 SVCPREGRLPPAKGAPHLRDIIFYRMGLTDKDIYALSGHSLGKAHPERSGPDGAWTRDP 180
DB 121 NVCPREGRLPPAKGAPHLRDIIFYRMGLTDKDIYALSGHSLGKAHPERSGPDGAWTRDP 180
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DB 181 LNFDSYFVRELKGESEGLLPTDKLTDPEFRRLVELYLA-DEDAFFDYAESHKRL 239
QY 240 SELGTPSSSGPASTKSYSTAVYLAOSAVYAAVYVINGLYLEASKRSK 291
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XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 7406.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.

XX EP1033405-A2.
PN 06-SEP-2000.
XX
PD 25-FEB-2000; 2000EP-0301439.
XX
PF 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 24-MAY-1999; 99US-0135629.
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PR 27-MAY-1999; 99US-0136382.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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Query Match 70.8%; Score 1061; DB 21; Length 254;
Best Local Similarity 77.1%; Pred. No. 1e-104;
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QY 94 LHOLAGVAVAEVYTGPTVEFIFGRDSSVCPREGRLPPAKKGAPLHRDIFRYMGITDKDI 153
DB 61 LYOLAGVAVAEVYTGPDIDYFVPRGRDSSVCPREGRLPPAKKGAFOHRLVFRMGISDKDI 120
QY 154 VALSGSHSLGKAHPERSGFGDAMTRDPLKFDNSYFLELLKGSEGLKLPDKALLDPE 213
DB 121 VALSGHHTLGRAHPERSGFGDAMTRDPLKFDNSYFLELLKGSEGLKLPDKALLDPE 180
QY 214 FRRYVELYAKKDEDFYFKDAESHKRLSELGTFPRSSGASRSDYSTAVLAQSAVGVAV 273
DB 181 FRRYVELYAKKDEDFYFKDAESHKRLSELGTFPRSSGASRSDYSTAVLAQSAVGVAV 236
QY 274 AAAYVAGTYEASKRSK 291
DB 237 AAAYVAGTYEASKRSK 254

RESULT 5
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AC AAG43317;
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DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 54128.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EPI033405-A2.
PD
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
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Query Match 70.8%; Score 1061; DB 21; Length 254;
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Matches 199; Conservative 27; Mismatches 28; Indels 4; Gaps 1;

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DB 1 MLRLAMHDAGTYDASQKGPNGSIRNEEHTHGANSGLIKTALDCEGAKAKHPKITTYAD 60
OY 94 LHOAGVAAVVTGGPTVEFTIPGRDSSVCPREGRLPDAKKGAPRLRDIIFYMGLTDDKI 153
DB 61 LYQLAGVAAVAVTGGPDIVFVPGKRDNSVCPREGRLPDAKKGQFOHLRDIIFYMGLSDKDI 120
OY 154 VALSGSHLGAHBERSGFDGAWTRDPLKFDNSYFLELLKGESEGLIKLPTDKALDDPE 213
DB 121 VALSGSHLGAHBERSGFDGAWTRDPLKFDNSYFLELLKGESEGLIKLPTDKALDDPE 180
OY 214 FRRYVELYADEDEVFKDYASHKLSLGLFTPRSSGPASTRKSDYSTAVVLAQSAVGVAV 273
DB 181 FRRYVELYADEDEVFKDYASHKLSLGLFTPRSSGPASTRKSDYSTAVVLAQSAVGVAV 236
OY 274 AAAYVYAGYLYEASKRSK 291
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AC AAG09702;
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XX 17-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
XX EPI03405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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Query Match	54.6%; Score 818.5; DB 21; Length 250;
Best local similarity 63.6%; Pred. No. 7.9e-79;	
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DB 6 PTVSEDKKAYEKCRRRLGLIAEKNKCAPIMVRLAWHSAGTDCSRTGSPGTMRFAE 65	PR 20-AUG-1999; 99US-0149722
QY 64 YTHCSNAGLKIADLLEPIKAKPKTTYADLNQAGVAVETGCPYVFIIRGRDSSVC 123	PR 20-AUG-1999; 99US-0149723
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AC AGI6805;
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17590.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PF 25-FEB-1999; 99US-0121825.
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QY	124	PREGRLPAKKGAPHLRDIETR-MGLDIDKIVALSGSHGAKAHERESSGFDGAWTRDPLK	182
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DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 30914.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter
XX	termination sequence.
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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OY 243 GF 244
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DB 246 GF 247

RESULT 9
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XX AAG43523;

XX AAG43523;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 54410.

XX Protein identification: signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

PN EP1033405-A2.

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PN	EP103405-A2.	99US-0127462
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XX		99US-0128714
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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PD 06-SEP-2000.
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KM	Protein identification; signal transduction pathway; metabolic pathway;		
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KM	termination sequence.		
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OY 243 GF 244
Db 293 GF 294

Search completed: October 23, 2002, 13:58:44
Job time : 34 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 14 Seconds
(without alignments)
804.814 Million cell updates/sec

Title: US-09-870-501-1

Perfect score: 1498
Sequence: 1 MAAPVYDAEYLROVDRARRA.....AVAAVYAGLYEASKRSK 291

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	802.5	53.6	249	1	APX1_PEA
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4	317	21.2	735	1	CAT4_BACST
5	294	19.6	737	1	CAT4_YERPE
6	280.5	18.7	731	1	CAT4_HALMA
7	276.5	18.5	720	1	CAT4_HAIIN1
8	272.5	18.2	749	1	CAT4_LEGNP
9	265	17.7	741	1	CAT4_ARCFU
10	257	17.2	726	1	CAT4_ECOLI
11	254.5	17.0	740	1	CAT4_SALTY
12	254	17.0	740	1	CAT4_MYCBO
13	254	17.0	740	1	CAT4_MYCNU
14	245.5	16.4	739	1	CAT4_MYCSM
15	244.5	16.3	737	1	CAT4_CAVCR
16	235.5	15.7	740	1	CATB_STRRE
17	232	15.5	752	1	CAT1_MYCFO
18	231.5	15.5	740	1	CATB_STRRO
19	226.5	15.1	746	1	CAT4_MYCIT
20	208.5	13.9	349	1	TL29_ARATH
21	201.5	13.5	378	1	PEM1_PHACH
22	201.5	13.5	382	1	PEM4_PHACH
23	201	13.4	345	1	TL29_LYCES
24	199.5	13.3	576	1	CAT4_RHOCA
25	187	12.5	292	1	PER2_CUCSA
26	171.5	11.4	347	1	PER2_ARMARU
27	171	11.4	322	1	PERX_ARMARU
28	170	11.3	364	1	PERX_ARMARU
29	167.5	11.2	363	1	PERX_ARMARU
30	167.5	11.2	305	1	PERX_ARMARU
31	166.5	11.1	330	1	PER2_ARMARU
32	164	10.9	296	1	PERX_ARMARU
33	162.5	10.8	332	1	PERX_ARMARU

RESULT 1	ID	APX1_ARATH	STANDARD:	PRT:	249 AA.
AC	005431;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (Ap).				
GN	APX1 OR AP1G07890 OR F24B9.2.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV, COLUMBIA;				
RX	MEDLINE=93138095; PubMed=8422923;				
RA	Kudo A., Saij H., Tanaka K., Kondo N.;				
RT	"Genomic DNA structure of a gene encoding cytosolic ascorbate				
RT	peroxidase from Arabidopsids thaliana.";				
RL	FEBS Lett. 315:313-317(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 1-16.				
RC	STRAIN=CV, COLUMBIA; TISSUE=Leaf;				
RX	MEDLINE=92216045; PubMed=1558944;				
RA	Kudo A., Saij H., Tanaka K., Tanaka K., Kondo N.;				
RT	"Cloning and sequencing of a cDNA encoding ascorbate peroxidase from				
RT	Arabidopsids thaliana.";				
RL	Plant Mol. Biol. 18:691-701(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV, COLUMBIA;				
RA	Tremousaygue D., Bardet C., Dabos P., Regad F., Pelese F.,				
RL	Lescure B.;				
RU	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV, COLUMBIA;				
RX	MEDLINE=21016719; PubMed=11130712;				
RA	Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,				
RA	White O., Alonso J., Atafati H., Araujo R., Bowman C.L., Brooks S.Y.,				
RA	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,				
RA	Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,				
RA	Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,				
RA	Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizlar L.,				
RA	Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,				
RA	Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,				
RA	Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,				
RA	Liu X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,				
RA	Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,				
RA	Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,				
RA	Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,				
RA	Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,				
RA	Uttelback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,				
RA	Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;				

ALIGNMENTS

34	161	10.7	316	1	PER1_ARMARU	P22195	arachis hyp
35	160.5	10.7	353	1	PERA_ARMARU	P00433	armoracia r
36	160	10.7	349	1	PERE_ARMARU	P24102	arabidopsids
37	158	10.5	324	1	PERX_TOBAC	P11965	nicotiana t
38	158	10.5	326	1	PER1_ARMARU	P37834	oryza sativ
39	155.5	10.4	312	1	PER1_ARMARU	Q05855	triticum ae
40	155.5	10.4	354	1	PERB_ARMARU	P24101	arabidopsids
41	151.5	10.1	351	1	PERB_ARMARU	P15232	armoracia r
42	149	9.9	372	1	LIG4_PHACH	P11542	panerochae
43	145	9.7	372	1	LIG4_PHACH	P20013	trametes ve
44	144.5	9.6	314	1	PER2_ARMARU	P37835	oryza sativ
45	137	9.1	349	1	PER3_ARMARU	P17180	armoracia r

```

DE 16-OCT-2001 (Rel. 40, last annotation update)
DE L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (AP).
GN APL1 OR APLX1.
OS Pistum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eumetids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pistum.
OX NCBI_TaxID=3889;
RN
RP SEQUENCE FROM N.A.
RP STRAIN-CV. LITTLE MARVEL; TISSUE=Leaf;
RC MEDLINE=92008636; PubMed=1915856;
RL Mitter R., Zilinskas B.A.;
RT "Molecular cloning and nucleotide sequence analysis of a cDNA
RT encoding pea cytosolic ascorbate peroxidase."
RN FEBS Lett. 289:257-259(1991).
RN
RP SEQUENCE FROM N.A.
RP STRAIN-CV. LITTLE MARVEL;
RC MEDLINE=93016138; PubMed=1400489;
RL Mitter R., Zilinskas B.A.;
RT "Molecular cloning and characterization of a gene encoding pea
RT cytosolic ascorbate peroxidase."
RN J. Biol. Chem. 267:21802-21807(1992).
RN
RP ERRATUM.
RA Mitter R., Zilinskas B.A.;
RL J. Biol. Chem. 268:4568-4568(1993).
RN
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RL Patterson W.R., Poulos T.L.;
RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLAYS A KEY ROLE IN HYDROGEN PEROXIDE REMOVAL IN
CC THE CHLOROPLASTS AND CYTOSOL OF HIGHER PLANTS.
CC -!- CATALYTIC ACTIVITY: L-ascorbate + H(2)O(2) = dehydroascorbate + 2
CC H(2)O.
CC -!- COFACTOR: HEME.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: BY STRESS.
CC -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. CYTOCHROME C
CC PEROXIDASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; M93051; AAA33645.1; -
DR EMBL; X62077; CAA43992.1; -
DR PDB; 1APX; 08-MAR-96.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS; PR00458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KM Oxidoreductase; Peroxidase; Hydrogen peroxide; Heme; 3D-structure.
FT INIT MET 0 0
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 41 41 DIGITAL HISTIDINE (BY SIMILARITY).
FT ACT_SITE 162 162 PROXIMAL HISTIDINE (HEME AXIAL LIGAND)
FT ACT_SITE (BY SIMILARITY).
SQ SEQUENCE 249 AA; 27061 MM; 6F43396D0A38442C CRC64;
Query Match 53.6%; Score 802.5; DB 1; Length 249;
Best local Similarity 62.8%; Pred. No. 2,2e-61;
Matches 152; Conservative 34; Mismatches 55; Indels 1; Gaps 1;

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QY      64   YTHSMNGLKTAIDLLLEPKRKHKKRTYYADHDLGAVVAEMVGGPFVEEIPGRSSVC    123
        ||::|||::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       65   LAHGANNCLDIAVRULEPIKQFPVIYADTYQLAGVAAVELTGGPVPHPGREDKEP    124
QY      124   PREGRLPAKKGAAPHLRDIFFR-NGLTDKDIALVSLSGSISAKAPERSGFDGAWTRDPLK    182
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       125   PREGRLPDATGSDHLRDVFESKANGSLDDQDIVALSNGTHIIGAANKHKSNGEGEPMTSNPLI    184
QY      183   FDNSTFELDLKGSEEGILKLPTDKALLDDPEFRRYVELYAKODEVFKDYAESHKRISEL    242
        |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       185   FDNSTFELLTLGEKDGLLOLPDSKALLTDTSVFEPLVEKYADEDEVFADYAEAHKLISEL    244
QY      243   GF 244
        ||
Db       245   GF 246

RESULT_3
CCPR_YEAST
AC      P00431;          STANDARD;          PRT;          361 AA.
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Cytochrome c peroxidase, mitochondrial precursor (EC 1.11.1.5) (CCP).
GN      CCP1 OR CCP OR CPO OR YKR066C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_Taxid=4932;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=D8788C.
RA      Platoni W., Miyazaki W., Jayaraman K., Kaput J.;
RL      Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=5288C.
RA      van Vleet-Reedijk J.C., Planta R.J.;
RL      Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=83082819; Pubmed=6294090;
RA      Kaput J., Goltz S., Blobel G.;
RL      "Nucleotide sequence of the yeast nuclear gene for cytochrome c
RT      peroxidase precursor. Functional implications of the pre sequence for
RT      protein transport into mitochondria.";
RL      J. Biol. Chem. 257:15054-15058(1982).
RN      [4]
RP      SEQUENCE OF 68-361.
RC      MEDLINE=61108305; Pubmed=6251776;
RA      Takio K., Titani K., Ericsson L.H., Yonetani T.;
RL      "Primary structure of yeast cytochrome c peroxidase. II. The complete
RT      amino acid sequence.";
RL      Arch. Biochem. Biophys. 203:615-629(1980).
RN      [5]
RP      SEQUENCE OF 253-332 FROM N.A.
RC      MEDLINE=82265845; Pubmed=6286684;
RA      Goltz S., Kaput J., Blobel G.;
RL      "Isolation of the yeast nuclear gene encoding the mitochondrial
RT      protein, cytochrome c peroxidase.";
RL      J. Biol. Chem. 257:11186-11190(1982).
RN      [6]
RP      X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RC      MEDLINE=85030410; Pubmed=6092361;
RA      Finzel B.C., Poulios T.L., Kreut J.;
RL      "Crystal structure of yeast cytochrome c peroxidase refined at 1.7-A
RT      resolution.";
RL      J. Biol. Chem. 259:13027-13036(1984).
RN      [7]
RP      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANTS.
RC      MEDLINE=91002554; Pubmed=2169873;
RX

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RA Wang J.M., Mauro M., Edwards S.L., Oatley S.J., Fishel L.A.,
RT Asiford V.A., Xiong N.-H., Kraut J.;
RT "X-ray structures of recombinant yeast cytochrome c peroxidase and
RT three heme cleft mutants prepared by site-directed mutagenesis.";
RL Biochemistry 29:7160-7173(1990).
CC -1 FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1 CATALYTIC ACTIVITY: 2 ferrocytochrome c + H(2)O(2) = 2
CC ferrocytochrome c + 2 H(2)O
CC -1 SUBUNIT: FORMS A ONE-TO-ONE COMPLEX WITH CYTOCHROME C.
CC -1 SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1 SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. CYTOCHROME C
CC PEROXIDASE SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X62422; CAA44288.1; -
DR EMBL; J01468; AAA88709.1; -
DR EMBL; J01321; AAA88710.1; -
DR EMBL; Z28291; CAA82145.1; -
DR PIR; S19064; OPRYC.
DR PDB; 2CYP: 15-APR-93.
DR PDB; 1CCP: 15-OCT-94.
DR PDB; 2CCP: 15-APR-93.
DR PDB; 3CCP: 15-APR-93.
DR PDB; 4CCP: 15-APR-93.
DR PDB; 5CCP: 31-OCT-93.
DR PDB; 6CCP: 31-OCT-93.
DR PDB; 7CCP: 31-OCT-93.
DR PDB; 2PCB: 15-JUL-93.
DR PDB; 2PCG: 15-JUL-93.
DR PDB; 1CCA: 31-OCT-93.
DR PDB; 1CCB: 31-OCT-93.
DR PDB; 1CCG: 31-OCT-93.
DR PDB; 1CCE: 31-JUL-94.
DR PDB; 1CCG: 31-JUL-94.
DR PDB; 1CCT: 07-JUL-97.
DR PDB; 1CCJ: 23-JUL-97.
DR PDB; 1CCK: 13-JAN-99.
DR PDB; 1CCL: 13-JAN-99.
DR PDB; 1CMP: 31-JAN-94.
DR PDB; 1CMO: 31-JAN-94.
DR PDB; 1CMT: 10-JUL-95.
DR PDB; 1CMU: 10-JUL-95.
DR PDB; 1DCC: 31-JUL-94.
DR PDB; 2CEP: 31-AUG-94.
DR PDB; 1CPD: 01-NOV-94.
DR PDB; 1CPE: 01-NOV-94.
DR PDB; 1CPF: 01-NOV-94.
DR PDB; 1CPG: 01-NOV-94.
DR PDB; 1A2F: 13-JAN-99.
DR PDB; 1A2G: 13-JAN-99.
DR PDB; 1AA4: 23-JUL-97.
DR PDB; 1AC4: 04-SEP-97.
DR PDB; 1AC8: 04-SEP-97.
DR PDB; 1AEB: 04-SEP-97.
DR PDB; 1AED: 04-SEP-97.
DR PDB; 1AEE: 04-SEP-97.
DR PDB; 1AEF: 04-SEP-97.
DR PDB; 1AEG: 04-SEP-97.
DR PDB; 1AEH: 04-SEP-97.
DR PDB; 1AEJ: 04-SEP-97.
DR PDB; 1AEK: 04-SEP-97.
DR PDB; 1AEM: 04-SEP-97.
DR PDB; 1AEN: 04-SEP-97.
DR PDB; 1AEO: 04-SEP-97.
DR PDB; 1AEO: 04-SEP-97.
DR PDB; 1AEO: 04-SEP-97.

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DR	PDB: 1AES; 04-SEP-97.	
DR	PDB: 1AET; 04-SEP-97.	
DR	PDB: 1AEU; 04-SEP-97.	
DR	PDB: 1AEV; 04-SEP-97.	
DR	PDB: 1ATC; 08-NOV-96.	
DR	PDB: 1CYF; 07-DEC-95.	
DR	PDB: 3CCX; 10-JUL-95.	
DR	PDB: 4CCX; 10-JUL-95.	
DR	PDB: 1BVA; 23-SEP-98.	
DR	PDB: 1BEJ; 21-OCT-98.	
DR	PDB: 1BEK; 21-OCT-98.	
DR	PDB: 1BEM; 21-OCT-98.	
DR	PDB: 1BEP; 21-OCT-98.	
DR	PDB: 1BEQ; 21-OCT-98.	
DR	PDB: 1BES; 21-OCT-98.	
DR	PDB: 1BJ9; 13-JAN-99.	
DR	SGD; S0001774; CCPI.	
DR	InterPro; IPR002016; Peroxidase.	
DR	Pfam; PF00141; peroxidase; 1.	
DR	PRINTS; PR00458; PEROXIDASE.	
DR	PROSITE; PS00435; PEROXIDASE_1; 1.	
DR	PROSITE; PS00435; PEROXIDASE_2; 1.	
KW	Oxidoreductase; Peroxidase; Heme; 3d-structure; Mitochondrion; Transist peptide; Polymorphism.	
FT	TRANSIT	1
FT	CHAMIN	67
FT	ACR_SITE	68 361
FT	ACR_SITE	115 115
FT	ACR_SITE	119 119
FT	ACR_SITE	242 242
FT	VARIANT	33 33
FT	VARIANT	120 120
FT	VARIANT	219 219
FT	MUTAGEN	258 258
FT	CONFLICT	41 41
FT	CONFLICT	62 62
FT	CONFLICT	145 146
FT	CONFLICT	231 231
FT	STRAND	74 74
FT	TORN	79 80
FT	HELIX	83 99
FT	TORN	100 102
FT	HELIX	103 106
FT	TORN	107 107
FT	HELIX	110 121
FT	TORN	122 123
FT	STRAND	125 125
FT	TORN	126 129
FT	STRAND	130 130
FT	TORN	134 135
FT	HELIX	137 139
FT	HELIX	141 144
FT	TORN	145 145
FT	HELIX	147 149
FT	TORN	150 152
FT	HELIX	153 165
FT	TORN	167 168
FT	HELIX	171 185
FT	HELIX	186 187
FT	STRAND	193 193
FT	HELIX	202 204
FT	TORN	218 226
FT	HELIX	227 229
FT	HELIX	232 243
FT	STRAND	246 247
FT	HELIX	249 252
FT	STRAND	256 257
FT	TORN	262 263
FT	HELIX	268 275
FT	STRAND	278 282
FT	TORN	284 285
FT	STRAND	288 292
FT	TORN	293 294
FT	STRAND	297 298

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FT      HELIX       300      307
Query Match          30.5%; Score 457; DB 1; Length 361;
Best Local Similarity 38.4%; Pred. No. 1.le-31;
Matches    93; Conservative   46; Mismatches 85; Indels 18; Gaps 3.

OY      GCATIMRLAMHAPAGVDTVTGCA-NSISIVEEETHSGNAGLKTALIDLEPIKAKHP 87
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      29 GCAIIMRLAMHAPAGVDTVTGCA-NSISIVEEETHSGNAGLKTALIDLEPIKAKHP 87
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      108 GYGIVYLRLAMHTSGTMDKHNDNGSSGYGTFFKEFDPSPNAGIQNGFKFLPEIRKEP 167
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      88 KITVADILHOLAGVAVEVTEGPTVEIFEPGRDS--SVCPRGRDPAKKAPHILRDIFFR 145
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      168 WISSGDLEFLSGTAVAOEMQPKIPRCRGVRDTPEDTPPDNGRPLDADKADYRTFFOR 227
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      146 MGLLDKXIVALLSGHSLSGRAHERSCFDGAWMRDLKDNSYLELLELKG----- 195
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      228 LNMDDREVVALLMGHAHALGTHLKNSGESEPGWCAANNVFTEFYINLNEMPLEKKDANN 287
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      196 -----SEGILKLPTDKALLDDPEFRERYVLAKDEVDFFKYAESHKLSLGTFPPRSS 250
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      288 EQMMSKSKGMWLLETVDYSLIQDPPRYSLISTVEYANODDKRFKFSNAFKLELNGITFPKXA 347
Db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      251 PA 252
Db      |::|
OY      348 PS 349

RESULT 4
CATAL_BACST
ID      CATAL_BACST        STANDARD;             PRT;           735 AA.
AC      P1412;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DR      Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN      PERA OR CAT.
OS      Bacillus stearothermophilus.
OC      Bacteria, Firmicutes; Bacillus/Clostridium group;
OC      Bacilli/Staphylococcus group; Geobacillus.
OX      NCBI_TaxID=1422;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC      STRAIN=ATCC 8005 / JAM11001;
RX      MEDLINE=89359121; PubMed=2670897;
RA      Lopriest S., Negro S., Okada H.;
RT      "Cloning, nucleotide sequence, and expression in Escherichia coli of
RL      the Bacillus stearothermophilus peroxidase gene (peraA).";
RN      RL. Bacteriol. 171:4871-4875(1989).
RJ      [2]
REV     REVISIONS.
RA      Trakunaleamsai S., Alhara S., Miyai K., Suga Y., Yomo T., Negro S.,
RA      Urahe I.;
RL      Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99116998; PubMed=9920270;
RA      Matsura T., Miyai K., Trakunaleamsai S., Yomo T., Shima Y.,
RA      Miki S., Yamamoto K., Urahe I.;
RT      "Evolutionary molecular engineering by random elongation
RT      mutagenesis.";
RN      Nat. Biotechnol. 17:58-61(1998).
RL      [1]
CC      -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC      BROAD-SPECTRUM PEROXIDASE ACTIVITIES.
CC      -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC      -1- COFACTOR: TWO PROTOHEME IX GROUPS.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC      PEROXIDASE/CATALASE SUBFAMILY.
CC      -----
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ID	CAT	YERPE	STANDARD	PRT	737 AA
AC	O9X6B0				
DR	16-OCT-2001	(Rel. 40, Created)			
DR	16-OCT-2001	(Rel. 40, Last sequence update)			
DR	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Peroxi-dase/catalase	(EC 1.11.1.6) (catalase-peroxidase) (Antigen 5).			
GN	KATY OR YEO3319.				
OS	Yersinia pestis.				
OC	Bacteria; Proteobacteria; gamma sub-division; Enterobacteriaceae;				
OC	Yersinia.				
OX	NCBI_TaxID=632;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-KIM;				
RX	MEDLINE=99255535; PubMed=10322012;				
RA	Garcia E, Nedialkov Y.A., Elliott J., Motin V.L., Brubaker R.R.;				
RT	"Molecular characterization of katy (antigen 5), a thermoregulated				
RT	chromosomally encoded catalase-peroxidase of Yersinia pestis."				
RL	J. Bacteriol. 181:3114-3122(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CO-92 / Biovar Orientalis;				
RX	MEDLINE=21470413; PubMed=11586360;				

[illegible]

16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN Halosarcina marismortui (Halobacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Halosarcina.
OX NCBI_TaxID=2238;
RN [1]
RP SEQUENCE FROM N.A.
RA Franzetti B., Cannac-Caffrey V., Petillot Y., Hudry-Clergeon G.,
RA Gagnon J., Zaccal G.,
RU Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) -> OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Y16851; CAAT6423.1; -.
DR HSSP: P00431; ICCK.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
FT ACT_SITE 92 92 BY SIMILARITY.
FT ACT_SITE 96 96 BY SIMILARITY.
FT BINDING 259 259 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 731 AA; 81383 MW; 0E12D0CF72FF3A3 CRC64;
Query Match 18.7%; Score 280.5; DB 1; Length 731;
Best Local Similarity 27.5%; Pred. No. 3.4e-16;
Matches 92; Conservative 39; Mismatches 88; Indels 115; Gaps 11;
QY 32 PIMRLAMHDGTY-DVNTFRGGANGSTRYEETVTHGNSAGLTKAIDLEPIKAKH-PKI 89
DB 88 PLFIRMAWHSAGTYRTADRGGAAGRGQRFAPINSMPPNANIDKARILLPIKORYGOKI 147
QY 90 TYADLHOLAGVAAVEVGTGPTVEFIPGRDSSVCPRE-----GR 128
DB 148 SWADLMILAGVAAVEVGTGPTVEFIPGRDSSVCPRE-----GR 128
QY 121 -----SVCPR--EGRLPDANKGAPHLIDYFIRMGILDKDIAL-SCGSHSLGKAH- 166
DB 208 GLGASVYGLIYVNEGPGDN-PDEPAKAKIRQGTEDRAMNDKETAALAGHTGKVG 266
QY 167 ---PER-----SGFGANTRODLKNDSTFLEL 191
DB 267 ADDEENLGPPEAPLIEQGLGWMKNGSKGEMITSGIEGPTOSTPTEDMDGYINNL 326
QY 192 L-----KG-----ESEGLKLPTDKLLDPERFRAYE 219
DB 327 LDYWEPEKGGGAGMOMAPKSEELKNSVPDAHDPEKOTPMMLTTDIALKRPDYREVME 386
QY 220 LYAKDEDVFFKDYAESHKLS--ELGFTPRSSGP 251
DB 387 TFOENPMFEGMNAKAWYKLTFRDGRPRERFLGP 420
RESULT 7
CATA_HALN1 STANDARD; PRT; 720 AA.
AC 073955; Q9HHP5;

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase)
GN PERA OR VNC6294G.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091, 2242;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NRC-1; PLASMID=pNRC200;
RA MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairs G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorson V., Sirogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo T.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebbhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
RA "Genome sequence of Halobacterium species NRC-1.";
RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=H. salinarum;
RA Salin M.L., Long S.;
RU Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) -> OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: AE005159; AAC20931.1; -.
DR EMBL: AF069761; AAC23534.1; -.
DR HSSP: P00431; 1B39.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Plasmid;
KW Complete proteome.
FT ACT_SITE 79 79 BY SIMILARITY.
FT ACT_SITE 83 83 BY SIMILARITY.
FT BINDING 248 248 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 720 AA; 80476 MW; FB88823BCD3CB2E9 CRC64;
Query Match 18.5%; Score 276.5; DB 1; Length 720;
Best Local Similarity 27.1%; Pred. No. 7.3e-16;
Matches 91; Conservative 41; Mismatches 87; Indels 117; Gaps 11;
QY 32 PIMRLAMHDGTY-DVNTFRGGANGSTRYEETVTHGNSAGLTKAIDLEPIKAKH-PKI 89
DB 75 PLFIRMAWHSAGTYRTADRGGAAGRGQRLPPVDSWPDVNLKARRLMLPIKORYKRL 134
QY 90 TYADLHOLAGVAAVEVGTGPTVEFIPGRDSSVCPRE-----GR 128
DB 135 SMGDLIILAGVAAVEVGTGPTVEFIPGRDSSVCPRE-----GR 128

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OY 129 L-----PDAKKGAPHLRDIYRNGLTDKDVAL--SGSHSLGKA 165
DB 194 LKMPGLNTWGLIYVNEPEGNGEPDLEGSAKNIRESGKAMANDKEVALLAGHAFEGKY 253
OY 166 H-----PER-----SGFDGAMTRDPLKFDNSYFL 189
DB 254 HGDADDEBENVGAPPAAPLEKOGIGWENEFEGCKGPDITTSIEGEGMNTPTQWDMSTYVD 313
OY 190 ELL-----KG-----ESRGLKLPDRLALDDPEFRY 217
DB 314 NLEFEMEPKGGGAMQMTTKSGELNESAPGVQDPTDIEDVMMLTVALKNDPPYREV 373
OY 218 VELIYADEDFEKKYAESHKKL--SELGTPNNSGP 251
DB 374 LETFOENPREFOQSFSAWKYKLIHRDMGCPSEFLGP 409

RESULT 8
CATALLEGPN
ID CATALLEGPN STANDARD; PRT; 749 AA.
AC 09MKB9;
DE 16-OCT-2001 (Rel. 40, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN KATG.
OS Legionella pneumophila.
OC Bacteria: Proteobacteria: gamma subdivision; Legionellaceae group;
OC Legionellaceae: Legionella.
OX NCBI_Taxid=446;
RN [1]
RP SEQUENCE FROM N.A.
RA Amemura-Maekawa J., Watanabe H.;
RA STRAIN=Am511;
RT "Legionella pneumophila catalase-peroxidase gene.";
RL Submitted (SEP-1998) to the EMBL/Genbank/DDBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTOHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DB EMBL: AB017595; BAA78342.1; --
DB HSSP: P00431; IRYC.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00458; Peroxidase; 1.
DR PRINTS: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KM Oxidoreductase: Peroxidase; Iron; Heme; Hydrogen peroxide.
FT ACU_Site 104 104
FT ACU_Site 108 108
FT ACU_Site 270 270
FT BIOPING 749 AA; 82914 MW; 19E7931C472973C8 CRC64;
SQ SEQUENCE

Query Match 18.2%; Score 272.5; DB 1; Length 749;
Best Local Similarity 27.3%; Pred. NO. 1.7e-15;
Matches 89; Conservative 37; Mismatches 91; Indels 109; Gaps 9;
OY 32 PMLRLAMHDAGTYDVNTGGANGSI-RYEETHTGSNAGKIALDLEPIKAKI-PRI 89
DB 100 PLEIRSMWMAAGTYRIYDGRGANGGEQFAFQNSPMNDANLNDKARLLMPKIKOKGKRI 159
OY 90 TYADLHQLAGVAVVEVTGPGTYVEFTIPGRD-----SSVCPREGRL--- 129

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DB 160 SMADLLVLGNVAMESEMGFTTIGFAGGREDAWAENINMGESKWLSEKRODKGLERP 219
OY 130 -----PDAKKGAPHLRDIYRNGLTDKDVAL--SGSHSGKHA--- 166
DB 220 LAATWGLIYVNEPEGNGVDPPLAAAEKIRETGAMNDDEEVALLAGHAGKTRGAA 279
OY 167 -----PE-----RSGFDGAMTRDPLKFDNSYFL--- 191
DB 280 SGKYLGPAPAEAGIEQGGWKNYSYSGKGDITTSIEGEGAMTVPTTHSHNTLQNLFPN 339
OY 192 --LKGESEG-----LKLIPDKALLDDPEFRYELVA 222
DB 340 NWVKTSFGGALQWVPENSNASSMVPDAPDSKRHAPVMTLALKFPVYSKIAKRL 399
OY 223 KDQDFVKDYAESHKRLSELGTPRS 248
DB 400 DNEKFPDAPARAWFKLIHRDMGPRS 425

RESULT 9
CATALLEGPN
ID CATALLEGPN STANDARD; PRT; 741 AA.
AC 028050;
DE 16-OCT-2001 (Rel. 40, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN PERA OR AF2233.
OS Archaeoglobus fulgidus.
OC Archaea: Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_Taxid=2234;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RA MEDLINE=98049343; PubMed=9389475;
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.R., Peterson J.D.,
RA Richardson D.L., Kerevage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kalne B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTOHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
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CC -----
DB EMBL: AE000951; AAB89022.1; --
DB HSSP: P48534; IAPX.
DR TIGR: AF2233; --
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00458; Peroxidase; 1.
DR PRINTS: PS00436; PEROXIDASE_1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.

```

DR PROSITE: PS00435; PEROXIDASE_1; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
 FT Complete proteome.
 FT ACT_SITE 83 BY SIMILARITY.
 FT BINDING 87 BY SIMILARITY.
 FT BINDING 249 PROXIMAL HEME LIGAND (BY SIMILARITY).
 SO SEQUENCE 741 AA; 84854 MW; A931DF34F050FC63 CRC64;
 Query Match 17.7%; Score 265; DB 1; Length 741;
 Best Local Similarity 27.0%; Pred. No. 7.2e-15;
 Matches 99; Conservative 39; Mismatches 102; Indels 126; Gaps 14;
 QY 7 DAELYROY-----DRARRFRALIAK-----GCAPIMRLAMHDGTYDVNRTG 52
 DB 40 DDVYEEVNDLIDAVIRLKEIMRSSQDMWPADEFGHGLFRLMWSAGSYRIEDGRG 99
 QY 53 GA-NGSIRYEEETHSGNAGLKAIDLLEPIKAKH-PKIYVADHOLAGVAAVEVTC--- 107
 DB 100 GARDSIRPRPLNMPNDINLQKALRLNPIKRYGRKLSMADLIILAGTVAMEDMGVKL 159
 QY 108 -----GPRVEFIPIGRDSS-----VCPR-EGRLPD 131
 DB 160 FCFALGREDIFPPDESPDMPGPEEEMLTAKRKEKELEPPAATEMGLIYVNPBGCGNPD 219
 QY 132 AKKGAPHLADIFYRMGLTQKDIYAL-SGHSLSGKAH-----PE----- 168
 DB 220 PLGSAQELIVAFRRMGMDDEETVALIAGHAFCKGACGADPADYLGDPSSSPIEMOGLG 279
 QY 169 -----RSGFDGAWTRDPLKFPNSYF-----LELLK---GSEGLLK--- 201
 DB 280 KYNVGKSGSDFTSGLEVTWSPTRPKGINVIRLIFTYEWELKEKSPAKGNQVAADAPE 339
 QY 202 -----LPTDKALLDDPEFRYVELYAKDEVEFKDYASHKKLSLGLFT 245
 DB 340 IIPDAHDPKKHRRPMLTADIALRDEPERSKTARFLNPEDEFEKAFALAWYKL-----T 394
 QY 246 PRSGP 251
 DB 395 HRDMP 400
 RESULT 10
 CATA_ECOLI STANDARD; PRT; 726 AA.
 ID CATA_ECOLI STANDARD; PRT; 726 AA.
 AC P13029;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peroxidase/catalase HPI (EC 1.11.1.6) (Catalase-peroxidase)
 DE (Hydroperoxidase I).
 GN KATG OR B3942.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN 11
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88314956; PubMed=3045098;
 RA Triggs-Raine B.L., Dobie B.W., Mulvey M.R., Sorby P.A., Loewen P.C.;
 RT "Nucleotide sequence of katG, encoding catalase HPI of Escherichia
 coli.";
 RL J. Bacteriol. 170:4415-4419(1988).
 RN 12
 RP SEQUENCE OF 1-339 FROM N.A.
 RX STRAIN-K12 / MG1655;
 RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
 RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
 region from 87.2 to 89.2 minutes.";
 RL Nucleic Acids Res. 21:3391-3398(1993).
 RN 13
 RP SEQUENCE OF 309-726 FROM N.A.
 RX STRAIN-K12 / MG1655;

RX MEDLINE=94089392; PubMed=8265357;
 RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
 RA Daniels D.L.;
 RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
 region from 89.2 to 92.8 minutes.";
 RL Nucleic Acids Res. 21:5408-5417(1993).
 CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
 BROAD-SPECTRUM PEROXIDASE ACTIVITIES.
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) -> O(2) + 2 H(2)O.
 CC -1- COFACTOR: TWO PROTOHEME IX GROUPS PER TETRAMER.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- INDUCTION: BY HYDROGEN PEROXIDE.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
 PEROXIDASE/CATALASE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 HEME REGULATORY MOTIF (HRM).
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 CC
 DR EMBL; M21516; AAA24040.1; -;
 DR EMBL; L19201; AAB03074.1; -;
 DR EMBL; U00006; AAC43048.1; -;
 DR EMBL; AE000468; AAC76924.1; -;
 DR PIR; J50140; CSECHP.
 DR PIR; S40885; S40885.
 DR HSSP; P48534; IAPX.
 DR SWISS-2DPAGE; P13029; COLI.
 DR Ecogene; EG10511; katG.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PR00141; Peroxidase; 1.
 DR PRINTS; PR00458; PEROXIDASE.
 DR PROSITE; PS00435; PEROXIDASE_1; 1.
 DR PROSITE; PS00436; PEROXIDASE_2; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
 KW Complete proteome.
 KW ACT_SITE 102 BY SIMILARITY.
 FT ACT_SITE 106 BY SIMILARITY.
 FT BINDING 267 PROXIMAL HEME LIGAND (BY SIMILARITY).
 FT DOMAIN 15 HRM 1 (POTENTIAL).
 FT CONFLICT 621 A -> G (IN REF. 1).
 SO SEQUENCE 726 AA; 80023 MW; 24D32EBED5DE9BD6 CRC64;
 Query Match 17.2%; Score 257; DB 1; Length 726;
 Best Local Similarity 27.1%; Pred. No. 3.4e-14;
 Matches 91; Conservative 34; Mismatches 103; Indels 108; Gaps 10;
 QY 31 APTMLRLAMHDGTY-DVNTRTGANGSIRYEEETHSGNAGLKAIDLLEPIKAKH-PK 88
 DB 97 AGLEFIMAMHGATYRSIDRGAGRGQORFAPLNSWPDNVSLDKARLLMPTRKQGRK 156
 QY 89 IITYADLHOLAGVAAVEVTCGPTVEFIPIGRD-----SSVCPREGRLPAKKGAP 137
 DB 157 ISMADLFILAGVVALVLENSGFRFGAGREDVWEPDLDVNNMGDEKAWLTHHPELAKAP 216
 QY 138 -----HLRDIIFYRMGLTQKDIYAL-SGHSLSGKAH--- 166
 DB 217 LGATEMGLIYVNPBGPDHSGEPLSAAAIIRAFMGCMKMDDETVALLAGCHTLLCKTGAG 276
 QY 167 -----PE-----RSGFDGAWTRDPLKFPNSYFLELLKG 194
 DB 277 PLSNVPPEAPPIEEOGLGNASTYSGVGADAITSGLEVVTQPTQWSYFENLFKY 336
 QY 195 E-----SEGLLK-----LPTDKALLDDPEFRYVELYAKD 224
 DB 337 EWWQTRSPAGATQFAVYAPETIIPDPFSKKRKRTMYLTDLIRLRFDEFEKISRRLND 396
 QY 225 EDVFFKDYAESHKKLSLGLFTPRSS--GPASTKSDV 258

Query Match 17.0%; Score 254.5; DB 1; Length 726;
Best Local Similarity 25.7%; Pred. No. 5.5e-14;
Matches 96; Conservative 41; Mismatches 111; Indels 125; Gaps 11.

FT	CONFLICT	223	223	G -> D (IN REF. 1).
FT	CONFLICT	228	228	N -> T (IN REF. 1).
FT	CONFLICT	238	233	D -> N (IN REF. 1).
FT	CONFLICT	273	273	A -> P (IN REF. 1).
FT	CONFLICT	275	275	A -> R (IN REF. 1).
FT	CONFLICT	545	545	S -> H (IN REF. 1).
FT	CONFLICT	549	549	S -> H (IN REF. 1).
FT	CONFLICT	553	553	A -> P (IN REF. 1).
FT	CONFLICT	561	561	O -> H (IN REF. 1).
FT	CONFLICT	634	634	R -> K (IN REF. 1).
SO	SEQUENCE	726 AA;	79656 MW; 764BA4439E9FFAB CRC64;	
Query Match 17.0%; Score 254.5; DB 1; Length 726; Best Local Similarity 25.7%; Pred. No. 5.5e-14; Matches 96; Conservative 41; Mismatches 111; Indels 125; Gaps 11.				
QY	IMLRAMHWDACTY-DVNTRTGANGSIRYEERTGSNAGLKIAIDLEPIAKH-PKIT	90	:	: : : : : : : : : :
DB	LFIIRAWMGACGYRISIDRGAGRGQQGFAPLNPDPNVSLDKARLLMPIKOKYGOKIS	158	:	: : : : : : : : : :
QY	IADIIHLGVAAVEVTGGPTVEFIFGRD-----SSVCDEGRGLPDAKKGA--	137	:	: : : : : : : : : :
DB	WADLFILLAGNNVALENSGRTEFGAGRGREDVMEPDLDVMKGDEKALJTHNHPLAKKAPLG	218	:	: : : : : : : : : :
QY	138 -----HLNDIYRMGLTDKDIAL-SGHSLSKAH-----	166	:	: : : : : : : : : :
DB	ATEMGLIYNPEGDPHGSEPLSAANAIRATGNMNMNEETVALTAGHTLCKTGAAAA	278	:	: : : : : : : : : :
QY	167 -----PE-----RSGFDDGWFRPDLPKFDNSYLELTKGE--	195	:	: : : : : : : : : :
DB	SHVGADPPAAAIIEAOGGLMASSYGSGVADAITSLLEVYYIOTPTQWSNYFPENLFKEYM	338	:	: : : : : : : : : :
QY	196 -----SEGRL-----LPTDKALLDPPERFRRYVELYAKDED	226	:	: : : : : : : : : :
DB	VOTRSPAPAIOFEAVDADDIIPDEPDPSKKRRKPMLVMDLTLRPDFEPFKISRRLFPDQ	398	:	: : : : : : : : : :
QY	227 VEFRDYANSHKKLS-ELGFTPRSSGPASTSDSVTAVALQ-----S	267	:	: : : : : : : : : :
DB	AFNEFAAEWAAMEKLHRDMGPARYTIGPEVPXEDLTWODPLPOLYPOEDIINKEALA	458	:	: : : : : : : : : :
QY	268 AVGVAAVAAVAIVIA	280	:	: : : : : : : : : :
DB	459 ASGLISEMSVYA	471	:	: : : : : : : : : :
RESULT 12 CATAL_MYCBO STANDARD: PRF: 740 AA. ID CATAL_MYCBO STANDARD: PRF: 740 AA. AC P46817; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DE Peroxidase/catalase (EC 1.11.1.6) (catalase-peroxidase). GN KATG. OS Mycobacterium bovis. OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. OX NCBI_TaxID=1765; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=BCG; RX MEDLINE=95264910; Pubmed=7746145; RA Heym B., Alzari P.M., Honore N., Cole S.T.; RT "Miscense mutations in the catalase-peroxidase gene, katG, are associated with isoniazid resistance in Mycobacterium tuberculosis."; RL Mol. Microbiol. 15:235-245(1995). CC CC - FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND INTRACELLULAR SURVIVAL OF MYCOBACTERIA (BY SIMILARITY). CC CC - CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O. CC CC - COFACTOR: TWO PROTOHEME IX GROUPS PER Tetramer. CC CC - SUBUNIT: HOMODIMER (PROBABLY). CC CC - SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL PEROXIDASE/CATALASE SUBFAMILY.				


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CC
DR EMBL: X83377; CAA58266.1; -.
DR HSSP: P00431; ICCA.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; Peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 108 108 BY SIMILARITY.
FT BINDING 270 270 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 740 AA; 80575 MW; 82310FF35397908 CRC64;
Query Match 17.0%; Score 254; DB 1; Length 740;
Best Local Similarity 25.6%; Pred. No. 6,3e-14;
Matches 99; Conservative 37; Mismatches 113; Indels 138; Gaps 12.
QY 32 PIMRLAHNHDACTYDVNTRTGGANGSI-RYEELYTHGSNAGLKIAIDLEPIKARH-PKI 89
Dy 100 PLFIAMWMAHAATYRIHIDRGSGAGGGMQFAPLNSWPDNASLDKARRLLMPYKKKYGKTL 159
QY 90 TYADHLOHQAIVAVAEVNTGGPIYELIPIGRD-----SSVCPRER 128
Dy 160 SWADLIVFRGNALCSMGKGTGFEPGRDQWDEPDEVYWGKEATYMGDERYSGKRDLENP 219
QY 129 L-----PDAKKGAP-----HLRDIFFRMGLTKDIDVAL-SGSHSLGRAH-- 166
Dy 220 LAAYQMGILYVPEAPNGPDPMAAAVIDIRETFRRMAAMNDVETALLVYGHTFGTHGAG 279
QY 167 -----PE-----KSGPDGANTROPPLKFDNSFYELFLKG 194
Dy 280 PADLVGPEPEAAPLEQMLGWRKSSYGTGTGKDAITSGLVVTNTPMKMDNS-FLEILYG 338
QY 195 ESEGLIKLP-----TDKALLDPPERARYVELYA 222
Dy 339 YEWELTKSPAGAMQYTAADKAGAGTIIPDFGPGKRSPTMLAIDLILNDPIYERITRRRL 398
QY 223 KDEVDFFEDYAESHKKL-SELGTFPRSSGP-----AST 254
Dy 399 EHPEELADEEFAAMWKLTHRDMPARYLGLPVKOTLMDQVPVAVSHDLVGEAEIASLV 458
QY 255 KSDVSTAVVLAQSAVGAIVAAAVVIAAG 281
Dy 459 KSOILASGLIVSQLVSTAMAAASSFRG 485
RESULT 13
CATA_MYCTU STANDARD: PRT: 740 AA.
AC Q08129: Q57274; Q57215; Q08221; Q50544; Q50546; Q50551; Q50552;
AC Q50553; Q50554; Q50555;
DT 01-OCT-1994 (Rel. 30, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase T (EC 1.11.1.6) (Catalase-peroxidase T).
GN KANG OR RV1908C OR MT1959 OR MTCY180.10.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN 1
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=H37RV;
RX MEDLINE=93308108; PubMed=8320241;

```

RA Heym B., Zhang Y., Poulet S., Young D., Cole S.T.;
RT "Characterization of the katG gene encoding a catalase-peroxidase
RT required for the isoniazid susceptibility of Mycobacterium
RT tuberculosis";
RL J. Bacteriol. 175:4255-4259(1993).
RN
RN (12)
RN REVISIONS.
RP STRAIN-H37RV;
RC Cole S.T.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN
RN (13)
RN SEQUENCE FROM N.A.
RP STRAIN-ATCC 25618;
RC Cockerill F.R., Ohl J.R., Temesgen Z., Zhang Y., Stockman L.,
RA Roberts G.D., Williams D.L., Kline B.C.;
RT "Rapid identification of a point mutation of the Mycobacterium
RT tuberculosis catalase-peroxidase (katG) gene associated with
RT isoniazid resistance.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN
RN (14)
RN SEQUENCE FROM N.A.
RP STRAIN-INH-RESISTANT STRAINS;
RC Mattila H.J., Soini H., Huovinen P., Viihinen M.K.;
RA "katG gene mutations in isoniazid-resistant Mycobacterium
RT tuberculosis strains isolated from Finnish patients";
RL Submitted (VAN-1996) to the EMBL/GenBank/DBJ databases.
RN
RN (15)
RN SEQUENCE FROM N.A.
RP STRAIN-H37RV;
RC MEDLINE=98295987; PubMed=6634230;
RA Cole S.T., Brosch R., Parthill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gess S., Barry C.E. III, Tekala F.,
RA Badoock R., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN
RN (16)
RN SEQUENCE FROM N.A.
RP STRAIN-CDC 1551 / Oshkosh;
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolony J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN
RN (17)
RN PARTIAL SEQUENCE FROM N.A., AND ISONIAZID RESISTANCE.
RP STRAIN-H37RV;
RC MEDLINE=92365822; PubMed=1501713;
RA Zhang Y., Heym B., Allen B., Young D., Cole S.T.;
RT "The catalase-peroxidase gene and isoniazid resistance of
RT Mycobacterium tuberculosis";
RL Nature 358:591-593(1992).
RN
RN (18)
RN SEQUENCE OF 1-94 FROM N.A.
RP STRAIN-H37RV;
RC Song J., Deretic V.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN
RN (19)
RN FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
RN BROAD-SPECTRUM PEROXIDASE ACTIVITIES. MAY PLAY A ROLE IN THE
RN INTRACELLULAR SURVIVAL OF MYCOBACTERIA.
RN
RN (20)
RN CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
RN
RN (21)
RN COFACTOR: TWO PROTONHEM IX GROUPS PER TETRAMER.
RN
RN (22)
RN SUBUNIT: HOMODIMER (PROBABLE).
RN
RN (23)
RN MISCELLANEOUS: DELETIONS OR DEFECTS IN KATG GENE CAUSE ISONIAZID
RN (INH) RESISTANCE.


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CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY, BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC or send an email to license@sdb.ch).
CC -----
DR EMBL: X68081; CAA48213.1; -
DR EMBL: 006258; AAB04159.1; -
DR EMBL: 040593; AAA85167.1; -
DR EMBL: 040595; AAA85169.1; -
DR EMBL: 041305; AAA85171.1; -
DR EMBL: 041306; AAA85172.1; -
DR EMBL: 041307; AAA85173.1; -
DR EMBL: 041308; AAA85174.1; -
DR EMBL: 041309; AAA85175.1; -
DR EMBL: 041310; AAA85176.1; -
DR EMBL: 041311; AAA85177.1; -
DR EMBL: 041312; AAA85178.1; -
DR EMBL: 041313; AAA85179.1; -
DR EMBL: 041314; AAA85180.1; -
DR EMBL: 297193; CAB10056.1; -
DR EMBL: AE007051; AAK46231.1; -
DR EMBL: AF002194; AAB63371.1; -
DR PIR: A40662; A40662.
DR PIR: S34036; S34036.
DR HSSP: P00431; 2PCB.
DR TIGR: MT1959; -.
DR Tuberculist; Rv1908c; -.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE_1; 1.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
DR Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
DR Complete proteome.
DR ACT_SITE 104 104 BY SIMILARITY.
DR ACT_SITE 108 108 BY SIMILARITY.
DR BINDING 270 270 PROXIMAL HEME LIGAND (BY SIMILARITY).
DR VARIANT 300 300 W -> G (IN INH-RESISTANT STRAIN
DR H0892/92).
DR VARIANT 315 315 S -> T (IN INH-RESISTANT STRAINS
DR H0181/94, H0452/92, H0948/92 AND
DR H0169/93).
DR VARIANT 463 463 R -> L (IN INH-RESISTANT STRAIN
DR H0169/93).
DR VARIANT 501 501 P -> A (IN INH-RESISTANT STRAIN
DR H0948/92).
DR VARIANT 525 525 O -> P (IN INH-RESISTANT STRAIN
DR H0251/90).
DR VARIANT 567 567 L -> P (IN INH-RESISTANT STRAIN
DR 15726/89).
DR VARIANT 700 700 S -> P (IN INH-RESISTANT STRAIN
DR H0004/93).
DR CONFLICT 234 234 G -> A (IN REF. 1).
DR SEQUENCE 740 AA; 80604 MW; B43C03B533CDD89 CR664;
Query Match 17.0%; Score 254; DB 1; Length 740;
Best Local Similarity 25.3%; Pred. No. 6,3e-14;
Matches 98; Conservative 36; Mismatches 115; Indels 138; Gaps 11;

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QY 129 L-----PDAAKGAPHLRDLIFYRMGLTDKQDVAL-SCGSHIGRAH---- 166
DB 220 LAAVGMGLIYVPEGNGNPDMAAAYVDIREFRRAANDVETALIVGCHTFGKTHGAG 279
QY 167 -----PE-----RSGFGANTROPLKDNSTFLELLG 194
DB 280 PADLVGPEPEAPLEQMGIGWSSYGTGKDAITSGIEVWMTNPETKWDNS-FLEILG 338
QY 195 ESEGLKLP-----DDKALLDPEFRRYELTA 222
DB 339 YEMELTFKSPAGAMQYAKKAGAGATIPDPFGGRSPFMLADLSLRVPYIERITRRRL 398
QY 223 KQEDVEFKDYASBHKKL--SELGFTPRSSGP-----AST 254
DB 399 EHPEELADEFAKAWYKLIHRDMGPVARYLGPVKQTLTMOPVPVASHDLVGEAEIASL 458
QY 255 KSDVSTAVVLAQSAVGVAANAAYVING 281
DB 459 KSOIRASGLTVSQLVSTAWAAASSFRG 485

RESULT 14
CAFA_MYCSM
ID CATP_MYCSM STANDARD; PRT; 739 AA.
AC Q59557; 005763;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Peroxidase/catalase T (EC 1.11.1.6) (Catalase-peroxidase T).
GN KATG.
OS Bacterium smegmatis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 700084 / MC(2)155;
RX MEDLINE=97023930; PubMed=8870251;
RA Billman-Jacobe H., Sloan J., Coppel R.L.;
RT "Analysis of isoniazid-resistant transposon mutants of Mycobacterium
RT smegmatis.";
RL FEMS Microbiol. Lett. 144:47-52(1996).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=MC(2)1216;
RA Engler O., Telenti A.;
RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES. MAY PLAY A ROLE IN THE
CC INTRACELLULAR SURVIVAL OF MYCOBACTERIA.
CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC -1- COFACTOR: TWO PROTOHEME IX GROUPS PER TETRAMER.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- MISCELLANEOUS: DELETIONS OR DEFECTS IN KATG GENE CAUSE ISONIAZID
CC (INH) RESISTANCE.
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY, BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
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DR EMBL: X98718; CAA67268.1; -
DR EMBL: 046844; AAC45275.1; -
DR HSSP: P48534; IAPX.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE_1; 1.
DR PROSITE: PS00435; PEROXIDASE_1; 1.

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DR PROSITE: PS00436; PEROXIDASE.2; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
 FT ACT_SITE 110 110 BY SIMILARITY.
 FT BINDING 114 114 BY SIMILARITY.
 FT PROXIMAL_HEME_LIGAND (BY SIMILARITY).
 FT CONFLICT 51 51 L -> M (IN REF. 2).
 FT CONFLICT 214 214 D -> RT (IN REF. 2).
 FT CONFLICT 374 374 PERITA -> AHEDG (IN REF. 2).
 SQ SEQUENCE 739 AA; 8113 MW; A15A754A826FBSD4 CRC64;
 Query Match 16.4%; Score 245.5; DB 1; Length 739;
 Best Local Similarity 26.2%; Pred. No. 3.3e-13;
 Matches 88; Conservative 37; Mismatches 98; Indels 113; Gaps 10;
 QY 32 PIMRLAMHDAGTYDVNTRTGGAN-GSIRYEETHTSGNAGLKAIIDLPEPIKAKHPK-I 89
 DB 106 PLFIRAMHAGTYRVSDDGAGAGAGMGRFAPLNSWPDNMSLDKARLLMPVKKKYKKNL 165
 QY 90 TYADHLQAGVAVETG-----GPTVEFTPGRRDSSVCPREG 127
 DB 166 SWADLIYVAGNALIEDMGFRTAGFARGREDRWEPEEDVYVPEQEWLDDKRYGERDLEN 225
 QY 128 RL-----PDARKGAPHLRDIIFYRMGLTDKIDVAL-SGSHSLGRAN-- 166
 DB 226 PLAAVOMGLIYVNEPGRNGNPDQASADIRETFGRAMANDVETALIVGHTFGKTHGN 285
 QY 167 -----PE-----RSGFDGAWTRDPLKEDNSYFLELTK 193
 DB 286 GDASLVGPEAPLEVEGLGWHNPOGTGVKDAITSGLEVTWTHPTKMDNS-FLIELY 344
 QY 194 GSEGLTKLP-----IDKALLDPEFRYVELY 221
 DB 345 GDEMELTKSPAGANQMKPKDNGWANSVPLPTKAKTHPSMLTSDLALRVDPIYEQITRRW 404
 QY 222 AKDEYFFKDYAESHKLL--SELGTPRSSGSPASTK 255
 DB 405 LDHPEELAEFAKAWFKLHRDMGPTRYLGPVEPK 440
 RESULT 15
 CATL_CAVCR STANDARD; PRT: 737 AA.
 ID CATL_CAVCR 031066;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
 GN KATG OR CC3043.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCRL_TaxID=69394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RA MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heldberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Pladek N.D., Ely B.,
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolony J.F., Smit J., Craven M.B., Kouri H., Shetty J., Berry K.,
 RA Usterback T., Tran K., Wolf A., Yamaliev J., Ermolova M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 RN [2]
 RP SEQUENCE OF 1-494 FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RA MEDLINE=98012985; PubMed=9352936;
 RA Steinman H.M., Fareed F., Weinstein L.;
 RT "Catalase-peroxidase of Caulobacter crescentus: function and role in
 stationary-phase survival.";
 RL J. Bacteriol. 179:6831-6836(1997).

CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
 CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES.
 CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
 CC -1- COFACTOR: TWO PROHEME IX GROUPS (BY SIMILARITY).
 CC -1- FUNCTION: TWO PROHEME IX GROUPS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
 CC PEROXIDASE/CATALASE SUBFAMILY.
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 CC -----
 CC EMBL: AE005967; AAC25005.1; -;
 CC EMBL: AF027168; AAC45850.1; -;
 CC HSSP: P00431; IRYC.
 CC TIGR: CC3043; -;
 CC InterPro: IPR002016; Peroxidase.
 CC Pfam: PF00141; peroxidase.1.
 CC PROSITE: PS00435; PEROXIDASE.1; 1.
 CC PROSITE: PS00436; PEROXIDASE.2; 1.
 CC Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
 CC Complete proteome.
 CC FT ACT_SITE 102 102 BY SIMILARITY.
 CC FT ACT_SITE 106 106 BY SIMILARITY.
 CC FT BINDING 268 268 PROXIMAL_HEME_LIGAND (BY SIMILARITY).
 CC SQ SEQUENCE 737 AA; 80165 MW; D900742D04E02E97 CRC64;
 Query Match 16.3%; Score 244.5; DB 1; Length 737;
 Best Local Similarity 26.4%; Pred. No. 4e-13;
 Matches 89; Conservative 37; Mismatches 98; Indels 113; Gaps 11;
 QY 33 IMRLAMHDAGTYDVNTRTGGAN-NGSIRYEETHTSGNAGLKAIIDLPEPIKAKHPK-PRIT 90
 DB 99 LFIRLAMHAGTYRITDGRGAGAGGQGFAPLNSWPDNMLDKARLLMPVKKKYKKNL 158
 QY 91 YADHLQAGVAVETGPTVEFTPGRRDSSVCPRE----- 126
 DB 159 WADLIYVAGNALIESMGFTFGFAGRADOME-PELLYNGPESTWLDKRYGERELDSP 217
 QY 127 -----GRL-----PDARKGAPHLRDIIFYRMGLTDKIDVAL-SGSHSLGRAN-- 167
 DB 218 LGAVOMGLIYVNEPGRNGNPDPLASARDIRETFGRAMANDVETALIVGHTFGKTHGN 277
 QY 168 -----ERSGFDGA-----WTRDPLKEDNSYFLELTK 194
 DB 278 DASLVGPEPAGALIEAGFGWASKHGTGKPDADITGSPVITWQPTFRSMHFFENLFRY 337
 QY 195 ESEGLTKLP-----TDKALLDPEFRYVELYAK 223
 DB 338 EWE-LTQSPAGAKOMAKNAPADIPDAPDNKTHVPRMLTSDLALRFPDPAVKISRRYE 396
 QY 224 DEDVFFKDYAESHKLLS--ELGTPRSSGSPASTKSDV 258
 DB 397 NPDQFADAFARAWFKLHRDMGPTRYLGPVEPKEL 433

Search completed: October 23, 2002, 13:56:44
 Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 14 Seconds

(without alignments)
507.703 Million cell updates/sec

Title: US-09-870-501-1

Perfect score: 1498
Sequence: 1 MAAPVDAEYLRQVDRARRA.....AVAAAVIAGLYEASRKRK 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCrUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	32.3	122	1	US-08-266-451B-18
2	484	32.3	122	2	US-08-748-725-18
3	454	30.3	294	2	US-08-459-499-16
4	451.5	30.1	293	2	US-08-313-185-52
5	451.5	30.1	293	3	US-09-082-614A-52
6	273.5	18.3	745	2	US-08-674-887A-8
7	273.5	18.3	745	3	US-08-951-844-8
8	272.5	18.2	753	2	US-08-674-887A-6
9	272.5	18.2	753	3	US-08-951-844-6
10	257	17.2	726	2	US-08-313-185-49
11	257	17.2	726	3	US-08-459-499-13
12	257	17.2	726	2	US-08-082-614A-49
13	254	17.0	740	1	US-08-418-782-7
14	254	17.0	740	1	US-08-418-782-21
15	254	17.0	740	1	US-08-228-662-7
16	254	17.0	740	2	US-08-852-219-7
17	254	17.0	740	2	US-08-852-219-21
18	247.5	16.5	729	2	US-08-313-185-50
19	247.5	16.5	729	2	US-08-459-499-14
20	247.5	16.5	729	3	US-09-082-614A-50
21	233	15.6	735	2	US-08-313-185-48
22	233	15.6	735	2	US-08-459-499-9
23	233	15.6	735	2	US-08-459-499-12
24	233	15.6	735	3	US-09-082-614A-48
25	219.5	14.7	652	2	US-08-313-185-53
26	219.5	14.7	652	2	US-08-459-499-11
27	219.5	14.7	652	3	US-09-082-614A-53

28	217	14.5	731	2	US-08-313-185-51	Sequence 51, Appl
29	217	14.5	731	2	US-08-459-499-15	Sequence 15, Appl
30	217	14.5	731	3	US-09-082-614A-51	Sequence 51, Appl
31	193.5	12.9	313	2	US-08-671-320-15	Sequence 15, Appl
32	193.5	12.9	313	3	US-08-868-577-15	Sequence 15, Appl
33	190.5	12.7	313	2	US-08-671-320-17	Sequence 17, Appl
34	190.5	12.7	313	2	US-08-868-577-17	Sequence 17, Appl
35	171	11.4	344	4	US-09-024-532-4	Sequence 4, Appl
36	171	11.4	345	1	US-07-792-259-12	Sequence 12, Appl
37	171	11.4	364	1	US-07-792-259-17	Sequence 17, Appl
38	170	11.3	343	2	US-08-624-545-1	Sequence 1, Appl
39	170	11.3	343	2	US-09-235-736-1	Sequence 1, Appl
40	170	11.3	363	1	US-08-458-023B-6	Sequence 6, Appl
41	170	11.3	435	2	US-08-331-515A-2	Sequence 2, Appl
42	170	11.3	435	4	US-09-168-406A-2	Sequence 2, Appl
43	156.5	10.4	349	1	US-08-190-029A-10	Sequence 10, Appl
44	156.5	10.4	349	2	US-08-462-695-10	Sequence 10, Appl
45	151	10.1	324	2	US-08-671-320-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-08-266-451B-18
; Sequence 18, Application US/08266451B
; Patent No. 5623054
; GENERAL INFORMATION:
; APPLICANT: Zhang et al.
; TITLE OF INVENTION: CIRCITER AFT PROTEINS AND USES
; NUMBER OF INVENTION: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,451B
; FILING DATE: 23-June-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/219001
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-5070
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-266-451B-18

Query Match      32.3%; Score 484; DB 1; Length 122;
Best Local Similarity 75.4%; Pred. No. 2.6e-45;
Matches 95; Conservative 9; Mismatches 18; Indels 4; Gaps 1;

QY 166 HPERSGFPGCAWRDRLKPFNSYLELKGESGLIKLPTDKALDDPEFRRLVETAYADE 225
DB 1 HPERSGFPGCAWRDRLKPFNSYLELKGESGLIKLPTDKALDDPEFRRLVETAYADE 60
QY 226 DVFFRDVAESHKKLSLGLTTPRSSGPASTKSDVSTAVVLAQSAVGVAANAAYIAGTYAE 285
```

DB 61 DAFEDYASHKSLSELGENPNSSAGKA-----VADSTILLOSAFGVAVAAGFYFE 116
QY 286 ASKRSK 291
DB 117 IKRKMK 122

RESULT 2

US-08-748-725-18
; Sequence 18, Application US/08748725
; Patent No. 5859346

GENERAL INFORMATION:

APPLICANT: Zhang et al.
TITLE OF INVENTION: CROCIER APT PROTEINS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,725
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,451
FILING DATE: 23-June-1994
ATTORNEY/AGENT INFORMATION:

NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/219002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 122
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-748-725-18

Query Match 32.3%; Score 484; DB 2; Length 122;
Best Local Similarity 75.4%; Pred. No. 2, 6e-45;
Matches 95; Conservative 9; Mismatches 18; Indels 4; Gaps 1;

QY 166 HPERSGFGAWTRDPLKFDNSYFLELLGSEGLKLPDKALLDDEPRRYVELYAKDE 225
DB 1 HPERSGFGDPWTOEPLKFDNSYFLELLGSEGLKLPDKLTLLDEPRRLVELYAKDE 60
QY 226 DVEFDYAEHSHKSLSELGTPRSSGPASTKSDYSTAVTLAQSAGVAAVAVIAGLYE 285
DB 61 DAFEDYASHKSLSELGTPPNSSAGKA-----VADSTILLOSAFGVAVAAGFYFE 116
QY 286 ASKRSK 291
DB 117 IKRKMK 122

RESULT 3
US-08-459-499-16
; Sequence 16, Application US/08459499
; Patent No. 5871912

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart T.
APPLICANT: Young, Douglas B.

TITLE OF INVENTION: Nucleic Acid Probes, Sequences, and Methods
TITLE OF INVENTION: for Detecting Mycobacterium Tuberculosis Resistant to Isonl
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,499
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/875,940
FILING DATE: 30-APR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/929,206
FILING DATE: 27-MAY-1992
APPLICATION NUMBER: US 08/029,655

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495, 0110-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-459-499-16

Query Match 30.3%; Score 454; DB 2; Length 294;
Best Local Similarity 38.4%; Pred. No. 2e-41;
Matches 93; Conservative 46; Mismatches 85; Indels 18; Gaps 3;

QY 29 GCAPIMRLAMHDAGTYDVNTRTGA-NGSIRYEERTHGSNAGKLAIDLLEPIKARHP 87
DB 41 GYGPVLVIRLAWHSITGWKHDNTGSGSYGTFRKKEFNDSNAGLONGFLEPIHKKEFP 100
QY 88 KITAYLHLQAGVAVNEVCGPTVEITGRBDS--SYCRBERLDDAKKAPHLRDIYR 145
DB 101 WISSGDFSLGVTAAVOENQGRIPRCGRVDTPEDTTPDNGRLDDAKKDGAVTFEPR 160
QY 146 MGLTLDIYALSGHSLGKAHPSGFGDAMTRDPLKFDNSYFLELLGSEGLKLPDKALLDDEPRRYVELYAKDE 225
DB 161 LNNNDREYVALKGAHALGTHLKNISYBPGWGAANNVFTNEYTLWLLMDKLEKNANN 220
QY 196 -----SEGLIKLPDKALLDDEPRRYVELYAKDEVEFKDYAESHKSLSELGTPRSSG 250
DB 221 EQWDSKSGYVMMLEPTDYSILQDPKYLSTYKEVANDQDFKDFSKAFKLENGITFPRDA 280
QY 251 PA 252
DB 281 PS 282

```
RESULT 4
US-08-313-185-52
; Sequence 52, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313.185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-313-185-52

Query Match          30.1%; Score 451.5; DB 2; Length 293;
Best Local Similarity 38.8%; Pred. No. 3.7e-41;
Matches 94; Conservative 46; Mismatches 83; Indels 19; Gaps 4;
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RESULT 5
US-09-082-614A-52
; Sequence 52, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313.185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-082-614A-52

Query Match          30.1%; Score 451.5; DB 3; Length 293;
Best Local Similarity 38.8%; Pred. No. 3.7e-41;
Matches 94; Conservative 46; Mismatches 83; Indels 19; Gaps 4;
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DB 401 RYENPDERADAFKAKMYKLTNRDGMCKYRYLGEPEVPOEDL 441

RESULT 8

US-08-674-887A-6
; Sequence 6, Application US/08674887A
; Patent No. 5939300
; GENERAL INFORMATION:
; APPLICANT: Robertson, Dan E.
; APPLICANT: Sanyal, Indrajit
; APPLICANT: Adhikari, Robert S.
; TITLE OF INVENTION: CATALASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,887A
; FILING DATE: 03-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09015/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-674-887A-6

Query Match

Best Local Similarity 18.2%; Score 272.5; DB 2; Length 753;
Best Local Similarity 27.0%; Pred. No. 6.4e-21;
Matches 93; Conservative 36; Mismatches 96; Indels 119; Gaps 10;

QY 33 IMRLAMHAGTYDY-NPTGGANGSIRYEEYTHGSNAGLAIADLEPIKAKH-PRIT 90
DB 120 IMIRAMHAGTYRRIADGGGGGTSORFAPLNSWPDNVLDKARLRLPIKKTGNKIS 179
QY 91 YADHLQAGVAVVEYTGPTVEIFGRD-----SSVCPREGRL----- 129
DB 180 WADLMILAGTAVYESMGLPAYGFSFGKVDIWEPEKDIYWGDEKEMLAPSDERYGVNKP 239
QY 130 -----PDAKGAPHLRDIFRMLGTLTKDIYAL-SGGHSLGK 164
DB 240 TMENPLAAVOMGLIYVNPBGVNGHDPRLTAQOVLETFARMAMNDEKTAALTAGGHTVGN 299
QY 165 AH-----PE-----RSGFDGAWTRDPLKFDNSYFL 189
DB 300 CHGNGNASALADPKRASDVENOGGLGNGNPMOGKASNAVTSGIEGAWTNPFTKFDGTF- 358
QY 190 ELLKGESEGLKLP-----TDKALIDPEFR 216
DB 359 DLLFGYNMELKSPAGAHMMEPIDIKENKPYDASDPSIRHNPIMTDADMAIKVNPTRYA 418
QY 217 YVELYAKDEDVFFKDYAESHKLS--ELGFTPRSSGPASTKSDV 258

DB 419 ICEKEMADPEYFKKTFAPKAMFKLTNRDLGPKSRYYIGPEVPARDL 462

RESULT 9

US-08-951-844-6
; Sequence 6, Application US/08951844
; Patent No. 6074860
; GENERAL INFORMATION:
; APPLICANT: Robertson et al.
; TITLE OF INVENTION: Catalases
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,844
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/674,887
; FILING DATE: July 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles J. Herron
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 331400-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1740
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: Polypeptide
; US-08-951-844-6

Query Match

Best Local Similarity 18.2%; Score 272.5; DB 3; Length 753;
Best Local Similarity 27.0%; Pred. No. 6.4e-21;
Matches 93; Conservative 36; Mismatches 96; Indels 119; Gaps 10;

QY 33 IMRLAMHAGTYDY-NPTGGANGSIRYEEYTHGSNAGLAIADLEPIKAKH-PRIT 90
DB 120 IMIRAMHAGTYRRIADGGGGGTSORFAPLNSWPDNVLDKARLRLPIKKTGNKIS 179
QY 91 YADHLQAGVAVVEYTGPTVEIFGRD-----SSVCPREGRL----- 129
DB 180 WADLMILAGTAVYESMGLPAYGFSFGKVDIWEPEKDIYWGDEKEMLAPSDERYGVNKP 239
QY 130 -----PDAKGAPHLRDIFRMLGTLTKDIYAL-SGGHSLGK 164
DB 240 TMENPLAAVOMGLIYVNPBGVNGHDPRLTAQOVLETFARMAMNDEKTAALTAGGHTVGN 299
QY 165 AH-----PE-----RSGFDGAWTRDPLKFDNSYFL 189
DB 300 CHGNGNASALADPKRASDVENOGGLGNGNPMOGKASNAVTSGIEGAWTNPFTKFDGTF- 358
QY 190 ELLKGESEGLKLP-----TDKALIDPEFR 216
DB 359 DLLFGYNMELKSPAGAHMMEPIDIKENKPYDASDPSIRHNPIMTDADMAIKVNPTRYA 418
QY 217 YVELYAKDEDVFFKDYAESHKLS--ELGFTPRSSGPASTKSDV 258

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Db      419 ICEKFNADDEYFKTFPAKAMFKLHRLDLPKRSRYIGPEVPAEDL 462
RESULT 10
US-08-313-185-49
: Sequence 49, Application US/08313185
: Patent No. 5851763
: GENERAL INFORMATION:
: APPLICANT: Heym, Beate
: APPLICANT: Cole, Stewart
: APPLICANT: Young, Douglas
: APPLICANT: Zhang, Ying
: APPLICANT: Honore, Nadine
: APPLICANT: Telenti, Amalio
: APPLICANT: Bodmer, Thomas
: TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
: TITLE OF INVENTION: In Mycobacterium Tuberculosis
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/313,185
: FILING DATE: 12-OCT-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Kenneth J.
: REGISTRATION NUMBER: 25,146
: REFERENCE/DOCKET NUMBER: 02356, 0068-00000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 408-4000
: TELEFAX: (202) 408-4400
: INFORMATION FOR SEQ ID NO: 49:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 726 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-313-185-49
Query Match      17.2%; Score 257; DB 2; Length 726;
Best Local Similarity 27.1%; Pred. No. 36-19;
Matches 91; Conservative 34; Mismatches 103; Indels 108; Gaps 10.
OY      31 APIMLPLAMHDAQTV-DVNTFRGANGASTIRYEBEYTHGSNAGIKTAIDLEPIKAKH-EK 88
      | : : : : | | | | | : : | : : : : | | | | | : : |
Db      97 AGLFLRMAMHGAGCTYRSIDRGAGACGQORFAPLNSWPDNVNSIDKARRILMPKQYCGOK 156
OY      89 ITYADLHLAGVYAVYEVGCTPVEFIPGRD-----SYVPRGRRLPDAKKGP 137
      | : : : | | | | | : : : | | | | | : : | | | | |
Db      157 ISWADFLTAGVVALENSQFRTFGAGREDVWEPDLDVNWGDDEKAMLTTHRPEALAKAP 216
OY      138 -----
      | : | | | | | | | | | | | | | | | | | | | | | |
Db      217 LGATEMGILYVNEPGRDHSGEPLSAAAATRAATFGNNGMNDDEETVALLAGSHLGTGHGK 276
OY      167 -----PE-----BSGFDGANTRPDLKEDNSYFELLNG 194
      | | | | | | | | | | | | | | | | | | | | | |
Db      277 PTSNPDPEAPRIEEQGLGMASIVYGSGVADATISGLEVTWTFPTQSNVYFEFLFYK 336
OY      195 E-----SEGLLK-----LPTDKALDDPEFRKRYVELIYAD 224
      | : : : : | : : : : | : : : : | : : : : | : : : :

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DB	337	EMVQTRSPGAIQIEFVADPEIIPDPBPSKKRKPMTLVTDLTLRDFEFKISRRLND	396
OY	225	EDVFEDVAKESHKKSJELGFTPRSS--GPASKSV	258
DB	397	POAFNEAFARAFWKLTLRDMGPKSRVIGPEVKEDL	432
		RESULT 11	
		US-08-459-499-13	
		; Sequence 13, Application US/08459499	
		; Patent No. 3871912	
		GENERAL INFORMATION:	
		APPLICANT: Heym, Beate	
		APPLICANT: Cole, Stewart T.	
		APPLICANT: Young, Douglas B.	
		TITLE OF INVENTION: Nucleic Acid Probes, Sequences, and Methods	
		TITLE OF INVENTION: for Detecting Mycobacterium Tuberculosis Resistant to Isonl	
		NUMBER OF SEQUENCES: 17	
		CORRESPONDENCE ADDRESS:	
		ADDRESSEE: Finegan, Henderson, Farabow, Garrett &	
		ADDRESSEE: Dunner	
		STREET: 1300 I Street, N.W.	
		CITY: Washington	
		STATE: DC	
		COUNTRY: USA	
		ZIP: 20005-3315	
		COMPUTER READABLE FORM:	
		MEDIUM TYPE: Floppy disk	
		COMPUTER: IBM PC compatible	
		OPERATING SYSTEM: PC-DOS/MS-DOS	
		SOFTWARE: Patent Release #1.0, Version #1.3	
		CURRENT APPLICATION DATA:	
		APPLICATION NUMBER: US/08/459,499	
		FILING DATE: 02-JUN-1995	
		CLASSIFICATION: 536	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: US 07/875,940	
		FILING DATE: 30-APR-1992	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: US 07/929,206	
		FILING DATE: 27-MAY-1992	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: US 08/029,655	
		FILING DATE: 11-MAR-1993	
		ATTORNEY/AGENT INFORMATION:	
		NAME: Meyers, Kenneth J.	
		REGISTRATION NUMBER: 25,146	
		REFERENCE/DOCKET NUMBER: 03495.0110-03000 *	
		TELECOMMUNICATION INFORMATION:	
		TELEPHONE: 202-408-4000	
		TELEFAX: 202-408-4400	
		INFORMATION FOR SEQ ID NO: 13:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 726 amino acids	
		TYPE: amino acid	
		TOPOLOGY: linear	
		MOLECULE TYPE: peptide	
		US-08-459-499-13	
		Query Match	17.2%; Score 257; DB 2; Length 726;
		Best Local Similarity	27.1%; Pred. No. 3e-19;
		Matches	91; Conservative 34; Mismatches 103; Indels 108; Gaps 10;
OY	31	APIMRLAMHDAQTY-DVNTRTGANGSIRREBEETHGSNAGLKAIDLEPIYAKH-PK	88
DB	97	AGLFIRAMHMGAGTYSIDRGAGRGQRAPLNSWPDNYSLLKARLLMPPIQYTGOK	156
OY	89	ITYADHLQAGVAEVEVGFPEIPIGRD-----SSVCPEGRULPAAKGGAP	137
DB	157	ISMADLTLAGNVALENSGFRFTFGGAGREDYWEPPDDVYMGDEKAMLTHTHPALAKAP	216

Db 100 PLEIRAMHAAGTYRIHDGSGAGGQRFAPLNSPDPNALSOKARLLMPVKKYKGL 159
Qy 90 TVADHLQAGVAVENTGCTPVEIFIGRD-----SSVCPREGR 128
Db 160 SMADLIIVFAGNCALIESGKFTGFGFGRVDQWEPDEYWGKEATWLDERYSGRDLENP 219
Qy 129 L-----PDARKGAPHLRDIYRMGLTDKDIYAL-SGSHSLGKAH--- 166
Db 220 LAAVQMLIYVNEGPNGNDPMAAAVDIRETFRAMANDVETALIVGGHFGKTHGAG 279
Qy 167 -----PE-----RSGFDGAWTRDPLKFDNSYFLELLG 194
Db 280 PADLVGPEPEAPLEQMGICGKSSYGTGCKDAITSGIEVWWTNPTKWDNS-FLEILYG 338
Qy 195 ESBGILLKP-----TDKALLDDEPFRRYVELYA 222
Db 339 YEWELTKSPAGAQYAKDAGAGTIPDPGPGRSPTMLATDLSLAVDPIYERITRRL 398
Qy 223 KDEDVFEKDYAESHKLL--SELGFTPRSSGP-----AST 254
Db 399 EHPEELADEFAKAKMYKLIRHDMGPVARYLGLPVKQTLMDQPVAVSHDLVGEAEIASL 458
Qy 255 KSDVSTAIVLAQSAVGVAANAAYVIAG 281
Db 459 KSOIRASGLTVSOLVSTAMAAASSFRG 485

RESULT 14
US-08-418-782-21

; Sequence 21, Application US/08418782
; Patent No. 5658733
; GENERAL INFORMATION:
; APPLICANT: Cockerill, Franklin R.
; APPLICANT: Kline, Bruce C.
; APPLICANT: Uhl, James R.
; TITLE OF INVENTION: Detection of Isoniazid Resistant Strains
; TITLE OF INVENTION: of M. Tuberculosis
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,782
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 150.141US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-782-21

Query Match 17.0%; Score 254; DB 1; Length 740;
Best Local Similarity 25.3%; Pred. No. 6.6e-19;
Matches 98; Conservative 36; Mismatches 115; Indels 138; Gaps 11;

Qy 32 PIMRLAMHDAGTYDVNTRTGANGSI-RYEEDYTHGSNAGLKIALIDLEPIKRAH-PKI 89
Db 100 PLEIRAMHAAGTYRIHDGSGAGGQRFAPLNSPDPNALSOKARLLMPVKKYKGL 159
Qy 90 TVADHLQAGVAVENTGCTPVEIFIGRD-----SSVCPREGR 128
Db 160 SMADLIIVFAGNCALIESGKFTGFGFGRVDQWEPDEYWGKEATWLDERYSGRDLENP 219
Qy 129 L-----PDARKGAPHLRDIYRMGLTDKDIYAL-SGSHSLGKAH--- 166
Db 220 LAAVQMLIYVNEGPNGNDPMAAAVDIRETFRAMANDVETALIVGGHFGKTHGAG 279
Qy 167 -----PE-----RSGFDGAWTRDPLKFDNSYFLELLG 194
Db 280 PADLVGPEPEAPLEQMGICGKSSYGTGCKDAITSGIEVWWTNPTKWDNS-FLEILYG 338
Qy 195 ESBGILLKP-----TDKALLDDEPFRRYVELYA 222
Db 339 YEWELTKSPAGAQYAKDAGAGTIPDPGPGRSPTMLATDLSLAVDPIYERITRRL 398
Qy 223 KDEDVFEKDYAESHKLL--SELGFTPRSSGP-----AST 254
Db 399 EHPEELADEFAKAKMYKLIRHDMGPVARYLGLPVKQTLMDQPVAVSHDLVGEAEIASL 458
Qy 255 KSDVSTAIVLAQSAVGVAANAAYVIAG 281
Db 459 KSOIRASGLTVSOLVSTAMAAASSFRG 485

RESULT 15
US-08-228-662-7

; Sequence 7, Application US/08228662
; Patent No. 5688639
; GENERAL INFORMATION:
; APPLICANT: COCKERILL, FRANKLIN R.
; APPLICANT: KLINE, BRUCE C.
; APPLICANT: UHL, JAMES R.
; TITLE OF INVENTION: DETECTION OF ISONIAZID RESISTANT STRAINS
; TITLE OF INVENTION: OF M. TUBERCULOSIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
; STREET: 3500 IDS CENTER
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,662
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WOESSNER, WARREN D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 150.123US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-228-662-7

Query Match 17.0%; Score 254; DB 1; Length 740;

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
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PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
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PR 01-JUN-1999; 99US-0137222.
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PR 30-JUN-1999; 99US-0141287.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
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PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154479.
PR 22-SEP-1999; 99US-0155139.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.

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PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 40.1%; Score 437; DB 21; Length 1157;
Best Local Similarity 69.6%; Pred. No. 2, 1e-116;
Matches 612; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

QY 16 GCGATGGCGGCTCCGGTGGTGGACGCCGAGTACTGCCGACGACGCGGCGCCG 75
DB 109 GCTATGGCTGACCGATTTGTGCGGAGTACTGAAAGATCTAAGGCTCCCGT 168
QY 76 GCGTTCGCGCCCTCATGCGCTCCCAAGGAGTGGCGCCCATCATGCTCCGCTCGCATGG 135
DB 169 GAGCTCCGTTCTCTCATCGCGAACAAGAACTGCTCTATCATGCTCGGATGGCATGG 228
QY 136 CATGATGCTGGACACTATGATGTGAACACAGAACTGTGTGTCATTAATTAATTA 195
DB 229 CACGATGCTGAACCTATGATGTCAATCGAAGACCGGTGACCTTAATGGCTCTATCAAG 288
QY 196 TACGAGGAAGATGACACCCATGTTTAAATGCTGCTTAAATTTGCTATGATCTCTT 255
DB 289 AACGAAGAAGACGACACTGTGTCGAACAGGTTTAAGATCCCTCGATCTCTGT 348
QY 256 GAGCCTATTAAAGCGAAGCATCAAGATTTACATATGACACCTTCATGCTTGGCGGA 315
DB 349 GAGGGGCTGAAGCTAAGATCCCAAAATCACATACGACACTGTATCATGCTGTGT 408
QY 316 GTAGTTCAGTTGAATGACACCGGGGTCCACCGTGTGAGTTTCCCTGGAAGACGTGAT 375
DB 409 GTGGTGAAGTGTGAGTGTCTGTGACCTGACATGCTGTGCTTCCCGGAGAAGAT 468
QY 376 TCGTCAATTTGCGCGGTGAAGACGCTTCTGATGCTAAGAGGTGACCAATCTA 435
DB 469 TCAATATGTGCCCCAAGAGAAAGACTTCCGATGCCAAACAGTTTCCAACTTC 528
QY 436 AGGACATCTTTATGAATGGGTTAACAACAAGATATTGTACCATATCTGGGGG 495
DB 529 AAGGATGCTTTCTACCGCATGGGACTATCTGATTAAGGATATTGCGACTCTCAGGGGT 588
QY 496 CACAGCCTGGGAAAGCGCATCTGAAAGTCTGGGTTTACGCGTACGATCTCTGAC 555
DB 589 CATACTCTGGAAAGGCTCACCGGAGAGTGTGAGGCTTTGATGAGCATGAGACCCAAAG 648
QY 556 CCTCTAAATTTGACAACATCACTTCTTGTGAGCTACTAAGGGGAATCTGAGGCTT 615
DB 649 CCGCTTAAATTTGACAACATCACTTCTGTAAGTCTGTAAGGAAATCAGAGGCTTG 708
QY 616 CTGAGCTCCCTGATGATGAGGATGTTGATGATGATCTGAATTTGAGGCTATGAGGAG 675
DB 709 TTGAAACTTCAACTGACAAAGACCTTATTGAGAGACCCGAGTTCGCTGCTGTGTGAG 768

QY 676 CTTTATGCAAGAGATGAGATGTTTCTTCAAGGACTACGCTGAATCACACAAAACCTT 735
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QY 736 TCTGAATGCTGCTTCAACGAGGACGATGCGCCGACATCTCAAAATCAAGTGTTC 795
DB 829 TCTGAGCTGTGTTTCAACCA-----ACTCTCAGCAGGCAAAACGATTTGA 876
QY 796 ACTGCTGTTGTACTTGCACAGATGTCAGTCCGAGTGTGAGAGTGTGACAGTGTATTC 855
DB 877 GACAGCAGCATCTGTGCAACAGATGCTGCGGCTTGCAGTGTCTGCTCGGTGTGGCA 936
QY 856 GCGGCTACCTGTACGAACTTCCAAAGAGAGCAAGTAA 894
DB 937 TTTGTTACTTTTACGAGATCCGAAAGAGATGAAGTAA 975

RESULT 2
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ID AAC34655 standard; DNA; 1160 BP.
XX
AC AAC34655;
XX
DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 7404.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.

PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138647.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
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PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
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PR	18-JUN-1999;	99US-0139750.
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PR	21-JUN-1999;	99US-0139817.
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PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
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PR	15-JUL-1999;	99US-0144005.
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PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0144886.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
<hr/>		
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	30-AUG-1999;	99US-0151080.
PR	31-AUG-1999;	99US-0151303.
PR	01-SEP-1999;	99US-0151348.
PR	07-SEP-1999;	99US-0151930.
PR	10-SEP-1999;	99US-0152363.
PR	13-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154409.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	22-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match 40.1%; Score 437; DB 21; Length 1160;
 Best Local Similarity 69.6%; Pred. No. 2.1e-116;
 Matches 612; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

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OY 16 GGGATGGCGGCTCCGGTGGTGGACGCCGAGTACCTGCCGAGGTGACAGCGGCGGCC 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 112 GCTATGGCTGCACCCATCTGTATGTCGGAGTACTTCAAGACGATCACTAAGGCTCT 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 76 GCGTCCGTCGCTCATGCTCCCAAGGATCGCCCGCATGCTCGCTCGCATG 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 172 GAGCTCCGTCCTCATGCTCGCAAGAACTGCTCCATCATGCTCGCATGCGATG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 136 CATGATGCTGCACTGATGATGTAACACAGAACTGCTGTCGAATGTTCAATTGA 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 232 CACGATGCTGGAACCTATGATGCTCAATGCAAGACCGGAGACCTAATGGCTCTATCAG 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 196 TACGAGAAAGATACACCCATGTTCAATGCTGGCTTAAATTTCTATTATCTCTT 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 292 AACGAAAGAGACACATCTATGTCGCAACAGTGGTTGAAGATGCTCTCATCTCTGT 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 256 GAGCTATTAAAGCAGACATCCAAAGATTACATATGACAGCTTCATGAGCTGCGGA 315
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 352 GAGGCGCTAAAGCTAAGATCCCAAAATCACATACGACGACCTGATACGCTTGCTGT 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 316 GATGTTGCAATTGAATGACCGGGGGTCCAAACGTTGAGTTCCTCCGGAAGAGCTGAT 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 412 GTGTATGACGTTGAGGTTACTGTGGTACATGCTGTGTTGCTCCGGGAAAGAT 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 376 TGTGATGTTGTCCCGGTGAAGAGCGCTTCTGATGCTAAGAAAGTGACCACTCA 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 472 TCAAAATGCTGCCCCAAGAAAGAACTCTGTATGCCAAACAGTTTCCAACTATC 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 436 AGGACATCTTTATGCAATGGGTTAAACAGCAAAAGATTATGTGACATATCTGGGGG 495
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 532 AAGATGCTTTTACCGCATGGGACTATCTGTAAGATATGTGGCACTCTCAGGGGT 591
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 496 CACAGCTGGGAAAGCGCATCTGAAAGGCTGAGGTTGACGGTGCATGACTGCTGTAC 555
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 592 CATACTCTGGAAAGGCTCACCCAGAGAGGTCAGGCTTGTATGAGCAATGACCAAGAG 651
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 556 CCTCGAATTGTTGACACATCACTCTCTGAGCTACCTGACAGGGGAATCTAGGCTCT 615
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 652 CCGCTGAAGTTTGAACACTCTACTCTGTTGAACTGCTGAAAGAGAAATCAGAGGGCTTA 711
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 616 CTGAAGCTCCCTACTGATTAAGCATTTGATGATCTGAAATTCGACGCTATGTGAG 675
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 712 TTGAACCTTCCAACTGACAGACACTTATTGGAAGACCGGAGTTCGCTGCTTGTGAG 771
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 676 CTTTATGCAAGGATGAGGATGTTTCTCAAGACTACGCTGAATCACAACAAAACCTT 735
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 772 CTTTATGCAAGGATGAGGATGTTTCTCAAGACTACGCTGAATCACAACAAAACCTT 831
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 736 TCTGAACCTGGCTTCACACACGAGCACTGCGCCAGATCTACAAATCAATGTTTCA 795
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 832 TCTGAGCTTGGTTTAAACCA-----AACTCCTCGACGAGCAAAACCACTATGCA 879
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 796 ACTGCTGTTTACTTGCACAGAGTCAAGTGGGATAGCAGTGTGACGCTGTATGATAC 855
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 880 GACACACGATTTCTGCGACAGAGTGCCTTGGGTTTGCAGTTGCTGCTGCGTTGTGCA 939
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 856 GCGGCTACCTTACGAAGCTTCCAAAGAGAGCAAGTAA 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 940 TTTGGTACTTTTACGAGATCCGGAAGAGATGAAGTAA 978
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 3
 AAA68052
 ID AAA68052 standard; DNA; 1080 BP.
 AC AAA68052;
 XX 24-OCT-2000 (first entry)

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XX DE Pinus radiata peroxidase nucleotide sequence SEQ ID NO:145.
XX XX Plant; Lignin; Lignin biosynthetic pathway; Eucalyptus grandis;
XX XX Pinus radiata; Monterey pine; ds.
XX OS Pinus radiata.
XX PN WO200022099-A1.
XX PD 20-APR-2000.
XX XX 06-OCT-1999; 99WO-NZ00168.
XX PF 09-OCT-1998; 98US-0169789.
XX PR 14-JUL-1999; 99US-0143811.
XX XX (GENE-) GENESIS RES & DEV CORP LTD.
XX PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX PI Bloksberg LN, Havukkala JU;
XX XX WPI: 2000-317962/27.
XX DR
XX XX Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
XX PT pathway useful for producing transgenic plants especially eucalyptus
XX PT and pine species having altered lignin content, composition and
XX PT structure -
XX PS Claim 1; Page 103; 213pp; English.
XX XX
XX CC The present invention describes isolated polynucleotides and proteins
XX CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),
XX CC cinnamate 3-hydroxylase (C3H), phenolase (PML), O-methyl transferase
XX CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
XX CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4Cl),
XX CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
XX CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
XX CC caffeine acid methyl transferase, caffeineoyl CoA methyl transferase,
XX CC coumarate CoA ligase, cytochrome P450 1XX1A, diphenol oxidase, flavanol
XX CC glucosyl transferase, flavanoid hydroxylase, and isoflavone reductase,
XX CC which are involved in the lignin biosynthetic pathway. The
XX CC polynucleotides can be used for modulating lignin content, lignin
XX CC composition and the structure of a plant, especially eucalyptus and pine
XX CC species, and for modifying the activity of an enzyme involved in lignin
XX CC biosynthetic pathway, and for producing a plant having altered lignin
XX CC content, composition and structure. They can be used for designing probes
XX CC and primers useful for detecting similar DNA and RNA sequences in any
XX CC organism and for PCR amplification. The lignin content can be efficiently
XX CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to
XX CC AAB16449 represent polynucleotide and protein sequences used in the
XX CC exemplification of the present invention.
XX SO Sequence 1080 BP; 287 A; 228 C; 268 G; 297 T; 0 other;

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Query Match 27.9%; Score 303.6; DB 21; Length 1080;
 Best Local Similarity 63.4%; Pred. No. 1.1e-77;
 Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

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OY 16 GCGATGGCGGCTCCGGTGGTGGACGCCGAGTACCTGCCCAAGTGCACAGGCGGCGCC 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 73 GTGAAGGCTTTATCCACCGCTAAGCGAGAGTACAAGGCTGCGCATGACAATGCAAGAG 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 76 GCGTCCGTCGCTCATGCTCCCAAGGATCGCCCGCATGCTCGCTCGCATG 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 AAGCTCCGAGCTCTCATTTGCAAGAGAACTGTGGCGCATCATGTTGTAATGCAATGG 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 136 CATGATGCTGCACTGATGATGTAACACAGAACTGCTGTCGAATGTTCAATTGA 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 193 CACAGCGCTGGGACTTACGATGATCAAGACCAAGCGGAGGCGCTTGGGAGCATGAGA 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 196 TACGAGAAAGATACACCCATGTTCAATGCTGGCTTAAATTTCTATTATCTCTT 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 253 TATGGGGCCGAGCTTCCCAACGCTGCTTAACAGTGTCTGACATTCGCACTTAGGCTCTG 312
QY 256 GAGCCTATTAAAGCAGACATCCAAAGATTATCATATGCAACCTTGATGACCTTGCCGGA 315
Db 313 GAGCCAAATCAAGAAAGATGTTCCCATTAATCATCCTTATGCTGATGATGAGTGGCTGGT 372
QY 316 GTAGTTGCAAGTTGAAGTCAACCGGGGCTTCAACCGTTGAGTTCATCCCTGGAACAGTGAT 375
Db 373 GTGGTGGCTGTTGAAAGTGAACGGGGGAGCTGACATTCCTGTCATCCCTGGAAGAGAAC 432
QY 376 TGTGAGTTGTGCTCCCGGAGAGAGCCTTCTGATGCTAAGAAAGGTGACCAACATCTA 435
Db 433 AAGCCTGAGACCTCCAGAAAGAGCCCTTCCGATGCTCAAAAGAGACCTGATCATCTG 492
QY 436 AGGCAATCTTTTATGAAATGGGGTTTACAGACAAAGATATTTAGCACTATCTGGGGGG 495
Db 493 AGGGATGTTTGTGTCATAGGGGTTGAAATGATAGAAATGTGGCCCTTGTCTGGTGCC 552
QY 496 CACAGCCTGGGAAAGGCGATCTCTGAAAGGTCTGGGTTTGGAGCGTGCATGACCTGTGAC 555
Db 553 CACACCTTGGGAGATGCCAAGAGAGATCTGTGTTTGAAGGACCTGAGCCTCTTAC 612
QY 556 CCTGTAATTTGACACATCATCTTCTTGAGCTACTGAAAGGGGAAATCTGAGGGCTT 615
Db 613 CCCCTTATCTTGGACAACTCTTACTTACAGAGCTTGTGACTGAGAGAGAGAGAGCCCTG 672
QY 616 CTGAAGCTCCTACTGATTAAGGCATTTGTGATGATCTGAAATTCGACGCTATGTGAG 675
Db 673 CTTCAGTTCCTCATCTGATTAAGGCATCTGCTGATGATCTAGTTTTCAGATTTATGTTCA 732
QY 676 CTTTATGCAAGAGATGAGATGTTTCTTCAAGSACTAGCCTGAATCACAACAAAACCT 735
Db 733 AAGTATGCAAGAGAGAAAGCCTTCTTCTGCTGACTATGCGAAGCTCACCTGAAGCTT 792
QY 736 TCTGAATCTGGCTT 749
Db 793 TCTGAATCTGGCTT 806

RESULT 4
AAV23904
ID AAV23904 standard; DNA; 1229 BP.
AC AAV23904;
XX 31-JUL-1998 (first entry)
DT
DE Plant POX enzyme DNA sequence.
XX
KW Lignin biosynthetic pathway; eucalyptus; pine; transgenic plant;
KW Lignin content; tree processing; cellulose fibre; ss.
XX
OS Pinus radiata.
XX
PN WO9811205-A2.
PD 19-MAR-1998.
PE 10-SEP-1997; 97WO-NZ00112.
PR 11-SEP-1996; 96US-0713000.
XX
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PI Bloksberg LN, Grierson AW, Havukkala JU;
DR WPI: 1998-207374/18.
XX
XX Sequences useful for modification of plant lignin content or
PT structure - from Eucalyptus grandis (eucalyptus) and Pinus radiata
PT (pine) are associated with lignin biosynthesis pathway, useful e.g.
PT in paper industry

XX
PS Claim 1; Page 68-69; 82pp; English.
XX
CC This sequence represents a fragment of the POX enzyme coding sequence. It
CC is an example of a DNA sequence of the invention, which are from
CC Eucalyptus grandis (eucalyptus) and Pinus radiata (pine) associated with
CC the lignin biosynthesis pathway. Constructs containing the DNA sequences
CC can be used to produce transgenic plants or plant cells, especially woody
CC plants e.g. eucalyptus or pine species but also e.g. monocotyledons or
CC dicotyledons; by stably incorporating the constructs into the plant
CC genome. The lignin content or structure, or activity of a specific enzyme
CC in the plant, can therefore be modulated. Reductions in lignin content or
CC changes in composition are useful in tree processing for paper. High
CC lignin content results in energy- and chemical-intensive separation
CC methods in order to obtain the pure cellulose fibre required. Reductions
CC in lignin content may also be useful for forage crops, whilst increases
CC or changes in composition may be desirable to increase the mechanical
CC strength of wood, change its colour or increase its resistance to rot.
CC The sequences are also useful as probes to isolate DNA sequences encoding
CC enzymes involved in the lignin biosynthesis pathway from other plant
CC species.
XX
SQ Sequence 1229 BP; 342 A; 256 C; 292 G; 339 T; 0 other:
Query Match 27.9%; Score 303.6; DB 19; Length 1229;
Best Local Similarity 63.4%; Pred. No. 1.2e-77;
Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;
QY 16 GCATGAGCGGCTCGGCTGTGAGCGCGGAGTACCTGCGCCAGTGCAGAGGCGCGCGC 75
Db 222 GTGAAGCTTTATCCCAACCTTAAGAGAGAGTACAGGCTCCATTCACAAATGCAAGG 281
QY 76 GCCTTCGTCGCTCCATCCCTCCAGAGGATGCGCCCATCATGCTCGGCTGCATG 135
Db 282 AAGCTCCGAGCTCTCATTCAGAGAAAGACTGTGGCCGATCATGTTGCAATGCAATG 341
QY 136 CATGATGCTGGACCATATATGTGAACACAAAGACTGTGGTGCAAAAGTTCAATTAGA 195
Db 342 CACAGGCTGGGAGCTTACATGATGCAAGACGAGGCGCTTGGGACGATGGA 401
QY 196 TACGAGAAAGATGACACCCATGTTCAAAATGCTGTTAAATGTAATTGATCTCTT 255
Db 402 TATGGGGCCGAGCTTCCCAACGCTGTAACAGTGTGTGACATGCGATTAAGCTCTG 461
QY 256 GAGCCTATTAAAGCAGACATCCAAAGATTATCATATGCAACCTTACATGCTGCGGA 315
Db 462 GAGCCAAATCAAGAAAGATGTTCCCATTAATCATCTGCTGACCTTATCAGTGGCTG 521
QY 316 GTAGTTGCAAGTTGAAGTCAACCGGGGCTCAACCGTTGAGTTATCTCCGGAAGCTGAT 375
Db 522 GTGGTGGCTGTTGAAGTGAACCGGGGAGCTGACATTCGTTCCATCTGGAAGAGAAC 581
QY 376 TGTGAGTTGTGCTCCCGGAGAGAGCCTTCTGATGCTAAGAAAGGTGACCAACATCTA 435
Db 582 AAGCCTGAGACCTCCAGAAAGAGCCCTTCTGATGCTACAAAGAGACCTGATCATCTG 641
QY 436 AGGCAATCTTTTATGAAATGGGGTTTAAACAGAAAGATATTTAGCACTATCTGGGGG 495
Db 642 AGGGATGTTTGTGTCATAGGGGTTGAAATGATAGAAATGTGGCTTGTCTGGTGCC 701
QY 496 CACAGCCTGGGAAAGGCGATCTCTGAAAGGTGTGGGTTTGAACGTTGACATGACCTGTGAC 555
Db 702 CACACCTTGGGAGATGCCAAGAGAGATCTGTTTGAAGGACCTGACCTTAC 761
QY 556 CCTGTAATTTGACAACTCATCTTCTGACTACTGAAAGGGGAGATCTGAGGGCTT 615
Db 762 CCCCTTATCTTGGACAACTCTTACTTACAGAGCTTGTGACTGGAGAGAAAGAGCCCTG 821
QY 616 CTGAAGCTCCTACTGATTAAGGCATTTGTGATGCTCTGAAATTTGCAAGCTATGTGAG 675
Db 822 CTTCAAGTTCATCTGATTAAGGCATGCTGCTGATCTAGTTTTCAGATTATGTTCA 881
QY 676 CTTTATGCAAGAGATGAGATGTTTCTTCAAGAGACTACGCTGAATTCACACAAAACCTT 735

[illegible]

Db	222	GTGAAGGCTTATCCCAACCGTAAAGCAGAGATGACAAAGCTGCCATTGACAAATGCAAGG	281
Qy	76	GCCTTCGGTCCCTCATCGCTCCCAAGGGATGCGCCCCCATCATGCTCCGCTCGCATGG	1359
Db	282	AAGCTCCGAGCTCTCATTTGCAAGAAAGATGTGGCCGATCATGGTTTCCAAATGCAATGG	3411
Qy	136	CATGATGCTGGCAGCTATGATGTGACACAAAGAACTGGTGGTGCATAATGGTTCAATTGA	1959
Db	342	CACACGCGCTGGGACTTACGATGTCAAGACCAAGACCGGAGGGCCCTTCGGGACGATGAGA	4010
Qy	196	TACGAGGAAGATACACCCATGGTTCAAATCTGGCTTAAAAATTTGCATTGATCTCTT	2555
Db	402	TATGGGCGGACCTTCCACCGGTGTCAACAGTGGTCTGGACATCGAGTAGTAGGCTCTTG	4610
Qy	256	GAGCCTATTAAAGCCAGACATCTCAAAAGATTTACATATGCAGACCTTCATCAGCTTGC	3150
Db	462	GAGCCATCAACAGAACATATTTCCCATATATCATCTATGTCAGCTTTATCAGTTGGCTGGT	5210
Qy	316	GTAATTGCAGTTGAAGTACCGGGGGGTCAAACCGTTGATGTCATCTCTGGAAGACGTAT	3750
Db	522	GTGGTGGCTGTGAAGTACCGGGGAGCTGACATTCGTTCCATCTCGAAGAGAGAC	5810
Qy	376	TGCTAGATTGTCCCCGGAGAGAGACGCTTCTGATGTGAAGAAAGTGCACCATCTGA	4350
Db	582	AAGCTGAGCCTCCAGAAAGAGGCGCCCTTCTGATGTCAAAAAAGACCTGATCATCTG	6410
Qy	436	AAGGACATCTTTATTCGATGGGGTTTAACAGACAAAGATATTATGACACTATCTGGGGGG	4950
Db	642	AAGGATGTGTTTTGGCTCACATGTGGGTTGATATATTAAGAAATTTGGCCCTTGTCTGGTGCC	7010
Qy	496	CACAGCCTGGGAAAGCGCATCTCGAAAGATCTGGGTTTGAAGGTGCATGGACTCGTAC	5550
Db	702	CACACCTTGGGGAGATGCGACAAAGAGATCTGGTTTTGAAGGACCATGGACCTCTAAC	7610
Qy	556	CCTCTGAAATTTGACAACTCATCTTTTGAAGTACTGAAGGGGGAATTCGAGGCTTT	6150
Db	762	CCCTTACTTCTTGACAACTCTTACTACAGAGCTGTGACTGGAGGAAGAGGCGCTG	8210
Qy	616	CTGAAGCTCCCTACTGATTAAGGCATTTGTGGATGTCCTGAAATTTGACGCTATGTGGAG	6750
Db	822	CTTTCAGTTGCCATCTGATTAAGGCACCTGCTTCTCATCTCACTTTTGGCATTTTATGTTCAG	8810
Qy	676	CTTTATGCAAGAGATGATGTTTTCTTCAAGGACTACGCTGATTCACAAAAAACTT	7350
Db	882	AAGTATGCAAGAGAGAGAGAGCGCTTTCTTCTGCTACATATGGGAAGCTCACCTGACGCTT	9410
Qy	736	TCTGAACCTTGGCTT 749	
Db	942	TCTGAACCTTGGGTT 955	
RESULT 6			
AAA67992			
ID	AAA67992 standard; DNA; 1229 BP.		
XX	AAA67992;		
XX	24-OCT-2000 (first entry)		
DE	Pinus radiata peroxidase nucleotide sequence SEQ ID NO:85.		
XX	Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;		
KW	Pinus radiata; Monterey pine; ds.		
XX	Pinus radiata.		
OS	WO200022099-A1.		
XX	20-APR-2000.		
PD	99WO-NZ00168.		
XX	06-OCT-1999;		
XX	09-OCT-1998; 98US-0169789.		
PR			

PR 14-JUL-1999; 99US-0143811.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLEET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX
PI Bloksberg LN, Hawukkala IJ;
XX
DR WPI; 2000-317962/27.
XX
XX Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
PT pathway useful for producing transgenic plants especially eucalyptus
PT and pine species having altered lignin content, composition and
PT structure -
PS
PS Example 2; Page 82; 213pp; English.
XX
XX The present invention describes isolated polynucleotides and proteins
CC encoding and representing the enzymes cinnamate 4-hydroxylase (CAH),
CC coumarate 3-hydroxylase (C3H), phenolase (PNU), O-methyl transferase
CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (ACL),
CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase,
CC coumarate CoA ligase, cytochrome P450 LKX1A, diphenol oxidase, flavanol
CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase,
CC which are involved in the lignin biosynthetic pathway. The
CC polynucleotides can be used for modulating lignin content, lignin
CC composition and the structure of a plant, especially eucalyptus and pine
CC species, and for modifying the activity of an enzyme involved in lignin
CC biosynthetic pathway, and for producing a plant having altered lignin
CC content, composition and structure. They can be used for designing probes
CC and primers useful for detecting similar DNA and RNA sequences in any
CC organism and for PCR amplification. The lignin content can be efficiently
CC modified using the polynucleotides. AAA67908 to AAA68201 and AAA16341 to
CC AAA16449 represent polynucleotide and protein sequences used in the
CC exemplification of the present invention.
XX
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SQ Sequence 1229 BP; 342 A; 256 C; 292 G; 339 T; 0 other;

Query Match 27.9%; Score 303.6; DB 21; Length 1229;
Best Local Similarity 63.4%; Pred. No. 1.2e-77;
Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

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DB 222 GTGAAGGCTTATCCACCTAGCGAGGAGTACAAAGCTGCCATTACAAATCAAGAGG 281
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DB 282 AAGCTCCGAGCTCTCTATTGACAGAAAGAACTGGCGCCGATGTTGCAATCGCATGG 341
QY 136 CATGATGCTGCGACCTATGATGTAACACAAAGAACTGCTGTCATATGATGTTCAATTAGA 195
DB 342 CACAGCGGTGGGACTTACATGTCAGACCAAGACCGGAGCGCCCTTGGGAGAGATGAGA 401
QY 196 TAGAGAAAGAGTACACCATGCTCAATGCTGCTTAAAAATTCCTATTGATCTCTT 255
DB 402 TATGGGGCCGACCTTGCACGAGTCTTAACAGTGTGTGACATCCAGTTAGGCTCTG 461
QY 256 GAGCTATTAAAGCAAGATCCAAAGATTACATATGACAGCTTATAGCTTGGCGGA 315
DB 462 GAGCCAAATCAAGAAAGTATCCCAATTAACCTATGATGATGATGATGATGATGATG 521
QY 316 GATGTTGAGTTGAAGTCAACGGGGGTCACACGTTGATGATGATGATGATGATGATGAT 375
DB 522 GTGGTGGCTGTGTAAGTCAACGGGGGTCACACGTTGATGATGATGATGATGATGATGAT 581
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DB 582 AAGCTGAGCCCTCAGAAAGAGCGCCCTTCTGATGCTAAGAAAGAGCTGATCATCTG 641
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DB 642 AGGATGTTTTTGTGCATCAGTGGGGTTGAATGATAAAGAAATGTGGCTTGTGTGTC 701
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DB 822 CTTGAGTTGCCATCTGATTAAGGCACTGCTGCTGATCTGATTTGCACTTATCTGACG 881
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS
OS Arabidopsis thaliana.
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PN EP103405-A2.
XX
PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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Query Match 24.7%; Score 269.4; DB 21; Length 1110;
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
PN EPI033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
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Query Match 24.7%; Score 269.4; DB 21; Length 1213;
Best Local Similarity 61.9%; Pred. No. 1e-67; Mismatches 271; Indels 3; Gaps 1;
Matches 445; Conservative 0;

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DB 268 GTGAGCCGAGTACCAAGAGGCTGTGGAGAGTGCAGAGCAAGCTCAGAGCTTGATC 327
QY 94 GCCTCCAGGATGCCGCCCATCATGTCGCCCTGCATGGCATGATGCTGGCACTAT 153
DB 328 GTGAGGAAGAACTGTCCACCATCATGTCGCGCATGCGATGCTGGAACTTTC 387
QY 154 GATGTGAACACAGACCTGCTGTGCAATGTTCAATTAGTACGAGGAGATACACC 213
DB 388 GATTGTCAATCAAGAGCTGAGGTGCATTCGGAACAAATGAGTTGAGCTGACCAACT 447
QY 214 CATGTTCAATCTGCGCTTAAATTTGCTATTGATCTCCTGAGCTATTAAAGCGAAG 273
DB 448 CATGAGCCCAACAGTGTATCCACATTTGCTTTAGTTGTTGGACCCCATCGGAGCA 507
QY 274 CATCAAAAGATTACATATCAGACCTTCATCAGCTTGCAGAGTATGCACTTGAAGTC 333
DB 508 TTCCCTACCATCTCTTGTGTGATTTCCATCAGCTTGCTGTGCGGCTGGAATTT 567
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Best Local Similarity 61.9%; Pred. No. 1e-67;
Matches 445; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

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DB 269 GTGAGCGAAGATTACAGAAAGGCTGTGAGAAAGTGCAGAGAGAGAGCTCAGAGCTTGTATC 328
QY 94 GCCTCCAGGAGATGCGCCCCATCATGCTCCGCTTCGATGCGCATGATGCTGGACCTAT 153
DB 329 GCTGAGAGAACTGTGCACCCATCATGTCCGATCGCATGCGACCTTCGTAACCTTTC 388
QY 154 GATGTACACAAAGAACTGGTGTGCAATGGTCAATTAGATAGAGAGAGATACAC 213
DB 389 GATTGTCAATCAAGACTGGAGGTCATTCCGAAACATGAGGTTTGACCTGAGAACT 448
QY 214 CATGTTCAATCTGCGCTTAAATTCATTTGATCTCCTTGAGCCATTAAAGCGAAG 273
DB 449 CATGAGCCCAAGGTGTATCCCATGCTCTTGAAGTGTGTGACCCCATCAGGAGCA 508
QY 274 CATCAAAAGATTACATATGACACTTCATCAGCTTCGCGGAGTGGTACAGTTAAGTC 333
DB 509 TTCCTTACCATCTCTTGTGATTTCCATCAGCTTGTGCTGTGGCCGTGAAGTT 568
QY 334 ACCGGGGGTCCAAAGCTGTAGTTTCATCCCTGGAAGACGTGATTCGATTTGTCCTCCT 393
DB 569 ACTGTGGCCCTGACATTCCTTTCACCTCGAAGAGAGAAACCCCAACCACTTCCA 628
QY 394 GAAGAGCCGCTTCGATGTAAGAAAGTGCACCATCTAAAGGACATCTT--TTAT 450
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DB 689 CAGATGGCTTATCTGACAAAGACATTTGCGCTTATTTGGGCCACACCTCTGGAGCA 748
QY 511 GCCCATCTGAAGGCTGTGGGTTTGACGGTGCATGACCTGACCCCTGGAATTTGAC 570
DB 749 TGCACAGAGATAGTCTGGCTTGAAGGTGCATGACATCAACCCCTTAATCTTTCGAC 808
QY 571 AACTCATCTTCTTGAGTACTGAAGGGGAATCGAGAGGCTCTCTGAAGCTCCCTTACT 630
DB 809 AACTCTTACTTCAAGAACTCTTGACGGAGAGAGAAAGGCTCTCTCAAGTTTCTCT 868
QY 631 GATAGGCATTTGTTGATATCTCTGAATTCGACGCTATGTGAGACTTATGACAAAGAT 690
DB 869 GACAAAGCACTATTGACACACCTGTTTCCGCTTTGTGTGAGAAATATACCTCTCAT 928
QY 691 GAGGATGTTTCTCAAGAGACTAGCTGATCAACCAAAAACTTGTGAATTTGGCT 749
DB 929 GAAGATGCTTTTCTGCTGATTAAGCTGAGGCCACATGAAAGCTTTCGAGCTTGGTT 987

RESULT 14
AAA68085
ID AAA68085 standard; DNA; 409 BP.
XX
AC AAA68085;
XX
XX 24-OCT-2000 (first entry)
DX
DE Pinus radiata peroxidase nucleotide sequence SEQ ID NO:178.

XX plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
KM Pinus radiata; Monterey pine; ds.
XX
OS Pinus radiata.
XX
PM WO200022099-A1.
XX
PD 20-APR-2000.
XX
PF 06-OCT-1999; 99WO-NZ00168.
XX
PR 09-OCT-1998; 98US-0169789.
PR 14-JUL-1999; 99US-0143811.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Bloksberg LN, Havukkala IJ;
XX
DR WPI; 2000-317962/27.
XX
XX
PT Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
PT pathway useful for producing transgenic plants especially eucalyptus
PT and pine species having altered lignin content, composition and
PT structure -
XX
PS Claim 1; Page 112; 213pp; English.
XX
CC The present invention describes isolated polynucleotides and proteins
CC encoding and representing the enzymes cinamamate 4-hydroxylase (C4H),
CC coumarate 3-hydroxylase (C3H), phenolase (PWL), O-methyl transferase
CC (OMT), cinammyl alcohol dehydrogenase (CAD), cinamoyl-CoA reductase
CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),
CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
CC caffeic acid methyl transferase, cateoyl CoA methyl transferase,
CC coumarate CoA ligase, cytochrome P450 1X1A, diphenol oxidase, flavanol
CC glucosyl transferase, flavonoid hydroxylase, and isoflavone reductase,
CC which are involved in the lignin biosynthetic pathway. The
CC polynucleotides can be used for modulating lignin content, lignin
CC composition and the structure of a plant, especially eucalyptus and pine
CC species, and for modifying the activity of an enzyme involved in lignin
CC biosynthetic pathway, and for producing a plant having altered lignin
CC content, composition and structure. They can be used for designing probes
CC and primers useful for detecting similar DNA and RNA sequences in any
CC organism and for PCR amplification. The lignin content can be efficiently
CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to
CC AAB16449 represent polynucleotide and protein sequences used in the
CC exemplification of the present invention.
CC
XX
SQ Sequence 409 BP; 101 A; 86 C; 112 G; 110 T; 0 other;

Query Match 19.4%; Score 211.6; DB 21; Length 409;
Best Local Similarity 73.1%; Pred. No. 3.4e-51;
Matches 285; Conservative 0; Mismatches 104; Indels 1; Gaps 1;

QY 303 TCAGCTTCGCCGAGTAGTTCAGTTGAATGACCGGGGCTCCACCGGTGATGATCC 362
DB 20 TCAGCCGGCTGGTGTAGTTGCTGTGAGTTACGGGAGGTCACACATTTGTTGCC 79
QY 363 TGAAGAGCTGATTCGTAGTTGTCGCCGTGAAGAGCGCTTCGTGATGATGAAGAG 422
DB 80 TGGTCGTAGAGTTCATCTGCATCACACGAGAGGCGCTTCGTGATGATGAAGAG 139
QY 423 TGCACACATCTAAGGAGCATCTTTATTCATGATGGGTTTAACAGCAAGATATGTAC 482
DB 140 TTCACAAACCTAAGGAGATCTTTTATAGATGGCCCTATCTGACAAAGATATGTTCC 199
QY 483 ACTATCTGGGGGGACAGC-CTGGGAAAGCGCATCTGAAGGCTGGGTTGAGCGGTG 541
DB 200 TCTTCTGAGGCGACACCATTTGGGAAAAGACATCCAGAAAGTGTCAGCTTGATGAG 259

QY 542 CATGACTCGTACCCCTCTGAAATTTGACACTCATCTTCTTGAGCTACTGAAGGGG 601
DB 260 CATGGACCGACGAGCCTCTGAAATTTGATTAATTTCTAGAGCTTCCAAAGCGG 319
QY 602 AATCTGAGGGTCTCTGAAGCTCCCTACATGAAGGCATTTGATGATCTGATTTTC 661
DB 320 AGCTGAAAGATTAATCTCCATTTGCTGAGGACAAATGCTTGGTAGGATCCAGTTTC 379
QY 662 GACGCTATGAGAGCTTTATGCAAGGATG 691
DB 380 GCCCTATCTGATCTTTATGCCAAGATG 409

RESULT 15
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ID AAC51668 standard; DNA; 687 BP.
XX
AC AAC51668;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69352.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PM EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
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PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132486.
PR 14-MAY-1999; 99US-0132486.
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PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
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 PR 28-OCT-1999; 99US-0161920.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 19.2%; Score 209.2; DB 21; Length 687;
 Best Local Similarity 63.4%; Pred. No. 2.3e-50;
 Matches 354; Conservative 0; Mismatches 195; Indels 9; Gaps 2;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 15:53:06 : Search time 1720 Seconds

(without alignments)
8545.456 Million cell updates/sec

Title: US-09-870-501-2

Perfect score: 1089
Sequence: 1 cttctaggtcgtccgcgat.....gaataaaaaaaaaaaaaa 1089

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estchum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	825.4	75.8	913	10	BF065877 HV_CEBD001
2	700.6	64.3	831	10	BE705572 SC01_03b1
3	678	62.3	703	9	AV936730
4	671.4	61.7	674	9	AV933174
5	664.4	61.0	675	9	AV927876
6	664	60.8	664	9	AV945933
7	662	60.8	662	9	AV929644
8	661	60.7	662	9	AV942984
9	660.4	60.6	666	9	AV937941
10	656.4	60.3	677	9	AV940735
11	639.2	58.7	863	10	BF254606 HVSMEF000
12	632.4	58.1	654	9	AV938146
13	631.4	58.0	652	9	AV934694
14	625.4	57.4	630	9	AV940226
15	623.4	57.2	630	9	AV909151
16	617.4	56.7	630	9	AV943215
17	617	56.7	665	9	AV922584

c	18	611	56.1	619	9	AV911034	AV911034
	19	605.8	55.6	622	9	AV917406	AV917406
	20	604.4	55.5	639	9	AV934079	AV934079
	21	604	55.5	604	9	AV909802	AV909802
c	22	601.4	55.2	614	9	AV927987	AV927987
	23	582.4	53.5	599	9	AV942033	AV942033
c	24	569	52.2	597	9	AV935664	AV935664
	25	566.8	52.0	829	10	BE417937	BE417937
	26	565.4	51.9	827	10	BF625164	BF625164
c	27	559.2	51.3	578	9	AV936329	AV936329
	28	557.4	51.2	591	9	AV912179	AV912179
	29	553	50.8	632	10	BF474988	BF474988
	30	551.8	50.7	556	9	AV932591	AV932591
c	31	546	50.1	667	10	BC904718	BC904718
	32	543.4	49.9	554	9	AV936963	AV936963
c	33	542	49.8	609	9	AV945334	AV945334
	34	537.4	49.3	548	9	AV935379	AV935379
c	35	537.4	49.3	580	9	AV924547	AV924547
	36	530.4	48.7	537	9	AV912284	AV912284
	37	524.4	48.2	527	9	AV933175	AV933175
	38	521.4	47.9	538	9	AV910104	AV910104
	39	513.8	47.2	726	9	BE214463	BE214463
	40	508.8	46.7	646	10	BF952074	BF952074
	41	504.4	46.3	589	10	BF478600	BF478600
	42	502.4	46.1	546	9	AV941025	AV941025
	43	498.4	45.8	652	9	AV923428	AV923428
	44	497	45.6	814	10	BE417956	BE417956
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
HV_CEBD014D20f Hordeum vulgare seedling green leaf EST library
HVCNDA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEBD014D20f, mRNA sequence.
BF065877.1 GI:10842516
ACCESSION
BF065877.1
VERSION
EST.
KEYWORDS
SOURCE
Hordium vulgare
barley.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 913)
Wing,R., Close,T.J., Kleinofcs,A., Wise,R., Wei,F., Begum,D., Fritsch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi ,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library
Unpublished (2001)
JOURNAL
Contact: Wing RA
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 653
Seq primer: AATTAAACCTCCTCAAGG
High quality sequence stop: 758.
FEATURES
source
1..913
Location/Qualifiers
/organism="Hordeum vulgare"
/cultivar="C116151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEBD014D20f"
/clone_lib="Hordeum vulgare seedling green leaf EST library HVCNDA0005 (Blumeria challenged)"

/tissue_type="seedling green leaf"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 C.I. 16151 (Ma6) Plants were greenhouse grown in the R
 wise lab at Iowa State University, Ames, IA; 7 day old
 green seedlings were challenged with isolate 5874 (AVRMA6
) of *Blumeria graminis* f. sp. hordei, and leaves were
 harvested 20 and 24 hr post-inoculation and snap frozen;
 uninoculated leaves were harvested 20 hr post-inoculation
 (Wel, Wise). In the R wise lab at the University of
 California, Riverside, total RNA was prepared from each
 sample pool, equal quantities of all three RNA pools were
 combined, poly(A) RNA was purified from the mixture, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give pBluescript SK(-) cDNA
 phagemids (Choi, Close). Phagemids were plated and picked
 at the Clemson University Genomics Institute (CUGI) (Begum
 Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close R, Wing R, Kleinhoft A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/gwpages/ggn/31/cover.html>)"

BASE COUNT 221 a 231 c 235 g 226 t
 ORIGIN

Query Match 75.8%; Score 825.4; DB 10; Length 913;
 Best Local Similarity 97.4%; Pred. No. 3.5e-157;
 Matches 860; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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 DB 33 CTTTAAAGGTCGTCGGGATGCGGCTCCGGTGTGAGCGCCAGTACCTGGCCAGGTC 92
 QY 61 GACAGGGGCGCGGCGCTCCGGTGTGAGCGCCAGTACCTGGCCAGGTC 120
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 DB 93 GACAGGGGCGCGGCGCTCCGGTGTGAGCGCCAGTACCTGGCCAGGTC 152
 QY 121 CTCGCGCTCGATGCGATGATGCGACCTATGATGTAACAAGAACTGGTGTGCA 180
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 DB 153 CTCGCGCTCGATGCGATGATGCGACCTATGATGTAACAAGAACTGGTGTGCA 212
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 DB 213 AATGTTCAATTAGATGAGAGAGAGTACACCATGTTCAATGCTGCTTAAAAATT 272
 QY 241 GCTATTGATCTCTGAGCTATTAAAGGAAGCATCAAGATTTCATATGCAACCT 300
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 DB 273 GCTATTGATCTCTGAGCTATTAAAGGAAGCATCAAGATTTCATATGCAACCT 332
 QY 301 CATCAGCTTGGCGAGTACCTGAGTTGAAGTCAACCGGGGCTCAACCGTTGAGTTTCA 360
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 DB 333 CATCAGCTTGGCGAGTACCTGAGTTGAAGTCAACCGGGGCTCAACCGTTGAGTTTCA 392
 QY 361 CCTGGAAGACGTGATTCGTCAGTTTCCCGTGAAGAGCGCTTCTGATGCTAAGAAA 420
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 DB 393 CCTGGAAGACGTGATTCGTCAGTTTCCCGTGAAGAGCGCTTCTGATGCTAAGAAA 452
 QY 421 GSTGACCACTAAGAGACATCTTTATCGAATGGGGTTAACAACAAGATATTGTA 480
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 DB 453 GSTGACCACTAAGAGACATCTTTATCGAATGGGGTTAACAACAAGATATTGTA 512
 QY 481 GCACATATCGGGGCGACAGCTTGGGAAGCGCATCTGAAGAGTCTGGGTTTGACGGT 540
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 DB 513 GCACATATCGGGGCGACAGCTTGGGAAGCGCATCTGAAGAGTCTGGGTTTGACGGT 572

QY 541 GCATGACCTGTGACCCCTTGAAATTTGACACTCATACTTCTTGAGCTACTGAGGG 600
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 DB 573 GCATGACCTGTGACCCCTTGAAATTTGACACTCATACTTCTTGAGCTACTGAGGG 632
 QY 601 GAATCTGAGGCTCTTGAGAGCTCCCTACGATGAAGCAATGTTGGATGATCTGAATT 660
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 DB 633 GAATCTGAGGCTCTTGAGAGCTCCCTACGATGAAGCAATGTTGGATGATCTGAATT 692
 QY 661 CGACGATGTGAGGCTTTATGCAAGAGATGAGATGTTTCTTCAAGAGTACCTGAA 720
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 DB 693 CGACGATGTGAGGCTTTATGCAAGAGATGAGATGTTTCTTCAAGAGTACCTGAA 752
 QY 721 TCACACAAAACTTCTTGAACTTGCTTCACACAGAGAGAGTGGCCAGCATCTACA 780
 |||||||
 DB 753 TCACACAAAACTTCTTGAACTTGCTTCACACAGAGAGAGTGGCCAGCATCTACA 812
 QY 781 AATTCAGATGTTTCAACTGCTGTGATGTCACACAGAGAGAGTGGCCAGCATCTGCT 840
 |||||||
 DB 813 AATTCAGATGTTTCAACTGCTGTGATGTCACACAGAGAGAGTGGCCAGCATCTGCT 871
 QY 841 GCACCTGATGTTTCGCGGCTACTGTACAGAGATCTTCCAGA 883
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 DB 872 GCAACTGTA-TTATTCGGGCTACCGGTCCAAAGTTCCAAA 913

RESULT 2
 BE705572/c 831 bp mRNA linear EST 12-SEP-2000
 LOCUS SC01.03b12.A SC01.AARC_ECORC_cold_stressed_winter_rye_seedlings
 DEFINITION Secale cereale cDNA clone SC01.03b12, mRNA sequence.

ACCESSION BE705572
 VERSION BE705572.1 GI:10093837
 KEYWORDS EST.
 SOURCE rye.
 ORGANISM *Secale cereale*

REFERENCE
 AUTHORS Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori
 J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
 Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
 Unpublished (2000)
 CONTACT: Singh,J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@em.agr.ca.

FEATURES
 source
 1..831
 Location/Qualifiers
 1..831
 /organism="Secale cereale"
 /cultivar="Puma (winter rye)"
 /db_xref="taxon:4550"
 /clone="Sc01_03b12"
 /clone_11b="Sc01.AARC_ECORC_cold_stressed_winter_rye_seedlings"
 /tissue_type="leaf, crown"
 /dev_stage="seedling three-leaf stage"
 /note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
 Site_2: Xho I; Sampled three-leaf seedlings treated for
 one week at 20c, 12 hrs light/day. Library made with
 Stratagene UNIZAP XR Kit/GigaPack III Gold Kit. Lambda
 library is amplified, then mass excised in SOLR cells."

BASE COUNT 234 a 199 c 168 g 229 t 1 others
 ORIGIN

Query Match 64.3%; Score 700.6; DB 10; Length 831;
 Best Local Similarity 95.6%; Pred. No. 6.6e-137;
 Matches 752; Conservative 1; Mismatches 30; Indels 4; Gaps 3;

QY 288 AATGCAAGACCTTCATCAGCTTCCGAGTACTGATGTAAGTACACGGGGGTCCAAC 347

[illegible]

JOURNAL COMMENT		Unpublished (2002) Contact: Tadasu Shln-1 Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tsbini@genes.nig.ac.jp. Location/Qualifiers	
FEATURES	source	1. .703	
		/organism="Hordium vulgare subsp. vulgare"	
		/cultivar="Haruna Nijo"	
		/db_xref="taxon:112509"	
		/clone="baal5k17"	
		/clone_id="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"	
		/issue_type="top three leaves"	
		/dev_stage="adult, heading stage"	
BASE COUNT	191 a 168 c 143 g 199 t	2 others	
ORIGIN			
Query Match	62.3%; Score 678; DB 9; Length 703;		
Best Local Similarity	99.6%; Pred. No. 2.5e-127;		
Matches 700; Conservative	0; Mismatches 1; Indels 2; Gaps 2.		
QY	364	GGAAAGCGTGAATTCGTCAAGTTGTCGCCCGTGAAGAGCGCCTTCGTATGCTTAAGAAAGCT	423
Db	703	GGAAAGCGTGAATTCGTCAAGTTGTCGCCCGTGAAGAGCGCCTTCGTATGCTTAAGAAAGCT	644
QY	424	GCACCAACATCTTAAGGACATCTTTATGAAATGGGGTTTAACAGACAAAGATTTGTAGCA	483
Db	643	GCACCAACATCTTAAGGACATCTTTATGAAAGGGGTTTAACAGAAAGATTTGTAGCA	584
QY	484	CTATCTGGGGGCAAGCGCTGGGAAAGCGCATCCCTGAAGAGGTCGGGTTGACGGTGCA	543
Db	583	CTATCTGGGGGCAAGCGCTGGGAAAGCGCATCCCTGAAGAGGTCGGGTTGACGGTGCA	524
QY	544	TGAGCTCGTGACCCCTCTGAATTTGACAACCTCATCTTCTTGAGCTACTGAAGGGGGA	603
Db	523	TGAGCTCGTGACCCCTCTGAATTTGACAACCTCATCTTCTTGAGCTACTGAAGGGGGA	464
QY	604	TCTGAGGGTCTTCTGAAGCTCCCTACTGATAAGCATTTGTTGATGATCTGTAATTTGCA	663
Db	463	TCTGAGGGTCTTCTGAAGCTCCCTACTGATAAGCATTTGTTGATGATCTGTAATTTGCA	404
QY	664	CGCTATGCGAGCTTTATGCAAGGATGAGGATGTTTCTTCAAGGACTAGCGCTGAATCA	723
Db	403	CGCTATGCGAGCTTTATGCAAGGATGAGGATGTTTCTTCAAGGACTAGCGCTGAATCA	344
QY	724	CACAAAAAATCTTCTGAAGCTGGCTTCACACACGAGCAGAGTGGCCCAACATCTACAAA	783
Db	343	CACAAAAAATCTTCTGAAGCTGGCTTCACACACGAGCAGAGTGGCCCAACATCTACAAA	284
QY	784	TCAGATGTTTCAACTGCTGTGTACTTTCACACAGATGCAAGTGGGGGTAGCAGTTCTGCA	843
Db	283	TCAGATGTTTCAACTGCTGTGTACTTTCACACAGATGCAAGTGGGGGTAGCAGTTCTGCA	224
QY	844	GCTGATTAATTCGGGGGTACTCTGACCAAGCTTCCCAAGAGGACGAAGTAAGGGTTCGT	903
Db	223	GCTGATTAATTCGGGGGTACTCTGACCAAGCTTCCCAAGAGGACGAAGTAAGGGTTCGT	164
QY	904	GAGTCTCTTGAGTGAATTCCTTATTTAGTAAGTATCAAGTATATTTCTAATAAAAAATTA	963
Db	163	GAGTCTCTTGAGTGAATTCCTTATTTAGTAAGTATCAAGTATATTTCTAATAAAAAATTA	104
QY	964	GTCGCCAAGTGCANAATACAGAACTCTAGTATGAACAACAACAGTAGTCTCAAAATATT	1023
Db	103	GTCGCCAAGTGCANAATACAGAACTCTAGTATGAACAACAACAGTAGTCTCAAAATATT	44
QY	1024	TCATACATTTCTTGAGGACATGCTCCTTCATATATATATACATCA 1064	
Db	43	TCATACATTTCTTGAGGACATGCTCCTTCATATATATATACATCA 1	

RESULT 4
LOCUS AV933174 674 bp mRNA linear EST 18-JAN-2002
DEFINITION AV933174 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal5k17 5', mRNA sequence.
ACCESSION AV933174
VERSION AV933174.1 GI:18228971
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
REFERENCE Sato, K., Saitoh, D. and Takeda, K. 1 (bases 1 to 674)
AUTHORS Sato, K., Saitoh, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 674
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="baal5k17"
/clone.lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"
/tissue.type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 159 a 165 c 187 g 163 t
ORIGIN
Query Match 61.7%; Score 671.4; DB 9; Length 674;
Best Local Similarity 99.9%; Pred. No. 5,4e-126;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 5 TAGGTCCTCCGCGATGCGGCTCGGCTGTGGAGCCCGACGATACCTGCGCCAGGTGAC 64
2 TAGGTCCTCCGCGATGCGGCTCGGCTGTGGAGCCCGACGATACCTGCGCCAGGTGAC 61
Y 65 GGGCGCGCGCGCTTCCTGCGCTCATGCGCTCCCAAGGATGCGGCCCATCATGCTCC 124
62 GGGCGCGCGCGCTTCCTGCGCTCATGCGCTCCCAAGGATGCGGCCCATCATGCTCC 121
Y 125 GCGTCGATGCGATGCTGCGACCTATGATGTGACACCAAGAACTGGTGTGCAATG 184
122 GCGTCGATGCGATGCTGCGACCTATGATGTGACACCAAGAACTGGTGTGCAATG 181
Y 185 GTTCAATTAGATAGAGAGAGATACCCATGCTTCAATGCTGGCTTAAATTTGCTA 244
182 GTTCAATTAGATAGAGAGAGATACCCATGCTTCAATGCTGGCTTAAATTTGCTA 241
Y 245 TTGATCTCTTGAGCTATTAAAGGAGATCCAAAGATTGATATGAGACCTTCATC 304
242 TTGATCTCTTGAGCTATTAAAGGAGATCCAAAGATTGATATGAGACCTTCATC 301
Y 305 AGCTTGCGGAGTAGTGTGAGTGAAGTACCGGGGTCACACCGTTGAGTTCATCCCTG 364
302 AGCTTGCGGAGTAGTGTGAGTGAAGTACCGGGGTCACACCGTTGAGTTCATCCCTG 361
Y 365 GAAGAGCGATTCGTCAGCTTTGTCCCGTGAAGAGCGCTTCTGATGCTAAGAAAGTG 424
362 GAAGAGCGATTCGTCAGCTTTGTCCCGTGAAGAGCGCTTCTGATGCTAAGAAAGTG 421
Y 425 CACCACTCTAAGGACATCTTTATCGAATGGGGTTAACAAGAAAGATTTGTAGCAC 484

Db 422 CACCACTCTAAGGACATCTTTATCGAATGGGGTTAACAAGAAAGATTTGTAGCAC 481
Y 485 TATCTGGGGGGCAGCAGCTGGGAAAGCGCATCTGAAAGGTCTGGTTGAGGTGAT 544
Db 482 TATCTGGGGGGCAGCAGCTGGGAAAGCGCATCTGAAAGGTCTGGTTGAGGTGAT 541
Y 545 GGACTGCTGACCTCTGAAATTTGACACTCATCTTTTGAAGCTACTGAAGGGGGAAT 604
Db 542 GGACTGCTGACCTCTGAAATTTGACACTCATCTTTTGAAGCTACTGAAGGGGGAAT 601
Y 605 CTGAGGCTCTTGAAGCTCCCTACTGATTAAGCATGTGGATGATCCTGAATTTGAC 664
Db 602 CTGAGGCTCTTGAAGCTCCCTACTGATTAAGCATGTGGATGATCCTGAATTTGAC 661
Y 665 GCTATGTGAGCT 677
Db 662 GCTATGTGAGCT 674
RESULT 5
LOCUS AV927876/c 675 bp mRNA linear EST 18-JAN-2002
DEFINITION AV927876 K. Sato unpublished cDNA library, cv. Haruna Nijo second leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA clone basd13b1 3', mRNA sequence.
ACCESSION AV927876
VERSION AV927876.1 GI:18223673
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
REFERENCE Sato, K., Saitoh, D. and Takeda, K. 1 (bases 1 to 675)
AUTHORS Sato, K., Saitoh, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 675
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="basd13b1"
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/tissue.type="seedling leaves"
/dev_stage="second leaf stage"
BASE COUNT 187 a 136 c 135 g 196 t 1 others
ORIGIN
Query Match 61.0%; Score 664.4; DB 9; Length 675;
Best Local Similarity 99.7%; Pred. No. 1,4e-124;
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 405 TCCGTATGCTAAGAAAGTGACACACATCTTAAGGACATCTTTATCGAATGGGTTAAC 464
Db 675 TCCGTATGCTAAGAAAGTGACACACATCTTAAGGACATCTTTATCGAATGGGTTAAC 616
Y 465 AGCAAAAGATTTATGACATCTATCTGGGGGACACAGCTCGGAAAGGGCATCTCGAAG 524
Db 615 AGCAAAAGATTTATGACATCTATCTGGGGGACACAGCTCGGAAAGGGCATCTCGAAG 556
Y 525 GTCTGGTTTGAAGGTCATGTCATCTGACCTCTGAATTTGACATCATACTTCT 584
Db 555 GTCTGGTTTGAAGGTCATGTCATCTGACCTCTGAATTTGACATCATACTTCT 496

QY 585 TGAGCTACTGAAGGGGAATCTGAGGCTCTTGAAGCTCCCTACTGATTAAGCATTGT 644
 Db 495 TGAGCTACTGAAGGGGAATCTGAGGCTCTTGAAGCTCCCTACTGATTAAGCATTGT 436
 QY 645 GGATGATTCCTGAATTCGACGCTATGTGAGCTTTTATGCAAGAGATGAGGATTTTCTT 704
 Db 435 GGATGATTCCTGAATTCGACGCTATGTGAGCTTTTATGCAAGAGATGAGGATTTTCTT 376
 QY 705 CAAGGACTAGCTGAATTCACACAAAAAATTTCTGAACCTTGCTGCACACGAGAGAG 764
 Db 375 CAAGGACTAGCTGAATTCACACAAAAAATTTCTGAACCTTGCTGCACACGAGAGAG 316
 QY 765 TGCCCCAGCATCTACAAATACAGATGTTTCACTGCTGTGTACTTGACAGAGTGTAGT 824
 Db 315 TGCCCCAGCATCTACAAATACAGATGTTTCACTGCTGTGTACTTGACAGAGTGTAGT 256
 QY 825 CGGGGTAGACGTTGCTGACGCTGATGTTATCGGGGCTACCTGTAGGAAGCTTCCAAAG 884
 Db 255 CGGGGTAGACGTTGCTGACGCTGATGTTATCGGGGCTACCTGTAGGAAGCTTCCAAAG 196
 QY 885 GAGCAAGTAAGGGGCTGAGTCTTGTGATGACATTCCTTATTTAGTAAATGATCAAGT 944
 Db 195 GAGCAAGTAAGGGGCTGAGTCTTGTGATGACATTCCTTATTTAGTAAATGATCAAGT 136
 QY 945 TATTATTTCTAAAAAATTAAGTCCCAAGTGCATAATTAACAGACTCTGTGATGACAAACA 1004
 Db 135 TATTATTTCTAAAAAATTAAGTCCCAAGTGCATAATTAACAGACTCTGTGATGACAAACA 76
 QY 1005 ACAGTGTCTCAAAATATTTCATACATTCCTGTGAGCATTCCTCATATATATATACATCA 1064
 Db 75 ACAGTGTCTCAAAATATTTCATACATTCCTGTGAGCATTCCTCATATATATATACATCA 16
 QY 1065 TACTTGA 1071
 Db 15 TACTTGA 9
 RESULT 6
 AV945933/c 664 bp mRNA linear EST 18-JAN-2002
 LOCUS AV945933 K. Sato unpublished cDNA library, strain H602 adult.
 DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
 accession CDNA clone ban29a06 3', mRNA sequence.
 VERSION AV945933
 KEYWORDS AV945933.1 GI:18241730
 SOURCE EST.
 ORGANISM Hordeum vulgare subsp. spontaneum.
 Hordeum vulgare subsp. spontaneum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 664)
 Sato, K., Saito, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished (2002)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1. 664
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602"
 /db_xref="taxon:77009"
 /clone="ban29a06"
 /clone_lib="K. Sato unpublished cDNA library, strain H602
 adult, heading stage top three leaves"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 BASE COUNT 183 a 155 c 134 g 192 t

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.7e-124;
 Matches 664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 404 TTCTGATGCTAAGAAAGGTGACACACATATTAAGGACATCTTTATCGAATGGGTTAA 463
 Db 664 TTCTGATGCTAAGAAAGGTGACACACATATTAAGGACATCTTTATCGAATGGGTTAA 605
 QY 464 CAGACAAAGATATTGTAGCACTATTCGGGGGGACAGACCCGGGAAAGGCGCATCTGAAA 523
 Db 604 CAGACAAAGATATTGTAGCACTATTCGGGGGGACAGACCCGGGAAAGGCGCATCTGAAA 545
 QY 524 GGTCTGGGTTTGAAGGTTGACATGACATCTGACCCCTGTAATTTGACAACTCATCTTTC 583
 Db 544 GGTCTGGGTTTGAAGGTTGACATGACATCTGACCCCTGTAATTTGACAACTCATCTTTC 485
 QY 584 TTGAGCTACTGAAGGGGGAATCTGAGGCTCTTGAGAGCTCCCTACTGATTAAGCATTTGT 643
 Db 484 TTGAGCTACTGAAGGGGGAATCTGAGGCTCTTGAGAGCTCCCTACTGATTAAGCATTTGT 425
 QY 644 TTGATGATCTGTAATTTGACAGCTATGAGGCTTTATGCAAGAGATGAGATTTTCT 703
 Db 424 TTGATGATCTGTAATTTGACAGCTATGAGGCTTTATGCAAGAGATGAGATTTTCT 365
 QY 704 TCAAGGACTACGCTGATATCACACAAAAAATTTCTGAACTTGGCTTCACACGAGACA 763
 Db 364 TCAAGGACTACGCTGATATCACACAAAAAATTTCTGAACTTGGCTTCACACGAGACA 305
 QY 764 GTGGCCAGCATCTACAAATTCAGATGTTTCAACTGCTGTGTACTTGACAGATGACAG 823
 Db 304 GTGGCCAGCATCTACAAATTCAGATGTTTCAACTGCTGTGTACTTGACAGATGACAG 245
 QY 824 TCGGGGTAGCAGTTGCTGACGCTGATGTTATCGGGGCTTCCTGACAGAGCTTCCAAG 883
 Db 244 TCGGGGTAGCAGTTGCTGACGCTGATGTTATCGGGGCTTCCTGACAGAGCTTCCAAG 185
 QY 884 GGAGCAAGTAAGGGGCTGAGTCTTGTGATGACATTCCTTATTTAGTAAGTATCAAG 943
 Db 184 GGAGCAAGTAAGGGGCTGAGTCTTGTGATGACATTCCTTATTTAGTAAGTATCAAG 125
 QY 944 TTTTATTTCTAAAAAATTAAGTCCCAAGTGCATAATTAACAGACTCTGTGATGACAAACA 1003
 Db 124 TTTTATTTCTAAAAAATTAAGTCCCAAGTGCATAATTAACAGACTCTGTGATGACAAACA 65
 QY 1004 AACAGTAGTCTCAAAATATTTCATACATTCCTGTAGGACATCTCTCATATATATACATC 1063
 Db 64 AACAGTAGTCTCAAAATATTTCATACATTCCTGTAGGACATCTCTCATATATATACATC 5
 QY 1064 ATAC 1067
 Db 4 ATAC 1
 RESULT 7
 AV929644/c 662 bp mRNA linear EST 18-JAN-2002
 LOCUS AV929644 K. Sato unpublished cDNA library, cv. Haruna Nijo second
 DEFINITION leaf stage seedling leaves Hordeum vulgare subsp. vulgare
 accession AV929644
 VERSION AV929644.1 GI:18225441
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare.
 ORGANISM Hordeum vulgare subsp. vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 662)
 Sato, K., Saito, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished (2002)

COMMENT

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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES

source

1. 662
/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Haruna Nijo"

/db_xref="taxon:112509"

/clone="basel4p20"

/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo second leaf stage seedling leaves"

/tissue_type="seedling leaves"

/dev_stage="second leaf stage"

BASE COUNT
ORIGIN

183 a 155 c 133 g 191 t

Query Match

Best Local Similarity 100.0%; Score 662; DB 9; Length 662;
Pred. No. 4.3e-124; Mismatches 0; Indels 0; Gaps 0;

Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 404 TTCCTATGCTAAGAAAGTGCACACATCTAAGGACATCTTTATCGAATGGGTTAA 463
DB 662 TTCCTATGCTAAGAAAGTGCACACATCTAAGGACATCTTTATCGAATGGGTTAA 603
OY 464 CAGACAAAGATATGTAGCTATCTGCGGGGACAGCCTGGGAAAGCGCATCCTGAA 523
DB 602 CAGACAAAGATATGTAGCTATCTGCGGGGACAGCCTGGGAAAGCGCATCCTGAA 543
OY 524 GGTCTGGGTTGACGGTGCATGACCTGACCCCTGAAATTTGACACTCATCTTC 583
DB 542 GGTCTGGGTTGACGGTGCATGACCTGACCCCTGAAATTTGACACTCATCTTC 483
OY 584 TTGAGCTACTGAAGGGGGAATCTGAGGGTCTTCTGAAGCTCCCTACTGATAGGCATTGT 643
DB 482 TTGAGCTACTGAAGGGGGAATCTGAGGGTCTTCTGAAGCTCCCTACTGATAGGCATTGT 423
OY 644 TGGATGATCCTGAATTTGACGCTATGTGAGGCTTTATGCAAGATGAGGATTTCT 703
DB 422 TGGATGATCCTGAATTTGACGCTATGTGAGGCTTTATGCAAGATGAGGATTTCT 363
OY 704 TCAAGGACTAGCGTGAATCACAACAAAACCTTTCTGAATTTGCTTCACACACGAGACA 763
DB 362 TCAAGGACTAGCGTGAATCACAACAAAACCTTTCTGAATTTGCTTCACACACGAGACA 303
OY 764 GTGGCCCAACATCTACAAAATCAGATGTTCAACTGCTGTTGTACTTGACACAGAGTCAG 823
DB 302 GTGGCCCAACATCTACAAAATCAGATGTTCAACTGCTGTTGTACTTGACACAGAGTCAG 243
OY 824 TGGGGGTAGCAGTTGCTGACAGTGTATTCGCGGGCTACTGTACGAAAGCTTCCAAAGA 883
DB 242 TGGGGGTAGCAGTTGCTGACAGTGTATTCGCGGGCTACTGTACGAAAGCTTCCAAAGA 183
OY 884 GGAGCAAGTAAGGGGTTCTGAGATCTTGTGATGACATTCCTTATTTAGTAAGATACAG 943
DB 182 GGAGCAAGTAAGGGGTTCTGAGATCTTGTGATGACATTCCTTATTTAGTAAGATACAG 123
OY 944 TTATTTATTTAAAAAATAGTCCCAAGTGCACAAATACAGAACTAGTATGACAAACC 1003
DB 122 TTATTTATTTAAAAAATAGTCCCAAGTGCACAAATACAGAACTAGTATGACAAACC 63
OY 1004 AACAGTAGTCTCAAAATATTTTACATCTTGAGGACATCTCCTCATATATATACATC 1063
DB 62 AACAGTAGTCTCAAAATATTTTACATCTTGAGGACATCTCCTCATATATATACATC 3
OY 1064 AT 1065
DB 2 AT 1

RESULT 8

AV942984/c

LOCUS

DEFINITION

AV942984 662 bp mRNA linear EST 18-JAN-2002
AV942984 K. Sato unpublished cDNA library, strain H602 adult.
heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone Dan15b23 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AV942984.1 GI:18238781
EST.
Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 662)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
unpublished (2002)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 662
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="Dan15b23"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
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/dev_stage="adult, heading stage" 1 others

FEATURES

source

1. 662
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
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/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage" 1 others

BASE COUNT
ORIGIN

180 a 155 c 134 g 192 t 1 others

Query Match

Best Local Similarity 99.8%; Score 661; DB 9; Length 662;
Pred. No. 6.8e-124; Mismatches 1; Indels 0; Gaps 0;

Matches 661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 406 CTTGATGCTAAGAAAGTGCACCAATCTAAGGACATCTTTATCGAATGGGTTAA 465
DB 662 CTTGATGCTAAGAAAGTGCACCAATCTAAGGACATCTTTATCGAATGGGTTAA 603
OY 466 GACAAGATTTGTAGACTATCTGGGGGCAAGGCTGGGAAAGCGCATCCTGAAAG 525
DB 602 GACAAGATTTGTAGACTATCTGGGGGCAAGGCTGGGAAAGCGCATCCTGAAAG 543
OY 526 TCTGGGTTTACGCGTGCATGACCTGTAACCTCTGAAATTTGACAACTCATCTTCT 585
DB 542 TCTGGGTTTACGCGTGCATGACCTGTAACCTCTGAAATTTGACAACTCATCTTCT 483
OY 586 GACCTACTGAAGGGGGAATCTGAGGCTCTTCTGAACTCCTACTGATAGGCATTGTG 645
DB 482 GACCTACTGAAGGGGGAATCTGAGGCTCTTCTGAACTCCTACTGATAGGCATTGTG 423
OY 646 GATGATCCCTGAATTTGAGGCTATGAGGCTTTTAAAGAGATGAGATTTTCTTC 705
DB 422 GATGATCCCTGAATTTGAGGCTATGAGGCTTTTAAAGAGATGAGATTTTCTTC 363
OY 706 AAGGACTAGCGTGAATCACAACAAAACCTTTGAACTGGGCTTCACACAGGAGCAGT 765
DB 362 AAGGACTAGCGTGAATCACAACAAAACCTTTGAACTGGGCTTCACACAGGAGCAGT 303
OY 766 GGCCCAACATCTCAAAATACAGATGTTCAACTGCTGTTGTACTTGACAGAGTCAGATC 825
DB 302 GGCCCAACATCTCAAAATACAGATGTTCAACTGCTGTTGTACTTGACAGAGTCAGATC 243
OY 826 GGGGTAGCAGTTGCTGACAGTGTATTCGCGGGCTACTGTACGAAAGCTTCCAAAGG 885
DB 242 GGGGTAGCAGTTGCTGACAGTGTATTCGCGGGCTACTGTACGAAAGCTTCCAAAGG 183

QY 886 AGCACTAAGGGGTTGAGTCTTGTGATGACATTCCTTATTTAGTATCAAGTT 945
|||||
DB 182 AGCACTAAGGGGTTGAGTCTTGTGATGACATTCCTTATTTAGTATCAAGTT 123
QY 946 ATTATTTCTAAAAAATTAAGTCCAGTCAATTAACAGACTCTAGTATGAACAACAA 1005
|||||
DB 122 ATTATTTCTAAAAAATTAAGTCCAGTCAATTAACAGACTCTAGTATGAACAACAA 63
QY 1006 CAGTAGTCTCAAAATTAATTCATACATTTCTTGAGGACATCCCTTCATATATACATCAT 1065
|||||
DB 62 CAGTAGTCTCAAAATTAATTCATACATTTCTTGAGGACATTCCTTCATATATATACATCAN 3
QY 1066 AC 1067
||
DB 2 AC 1
RESULT 9
AV937941 666 bp mRNA linear EST 18-JAN-2002
LOCUS AV937941 K. Sato unpublished cDNA library, strain H602 adult.
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
CDNA clone ban15d23 5', mRNA sequence.
ACCESSION AV937941 GI:18233738
VERSION AV937941.1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 666)
AUTHORS Sato, K., Saitoh, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
FEATURES
source
1. 666
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="ban15d23"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 156 a 165 c 182 g 163 t
ORIGIN
Query Match 60.6%; Score 660.4; DB 9; Length 666;
Best Local Similarity 99.8%; Pred. No. 1,le-124;
Matches 661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTCTTAGGGTGTCCGCGATGCGGCTCGGTGTGGAGCGCCAGTACCTGGCCAGGTC 60
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DB 5 CTCTTAGGGTGTCCGCGATGCGGCTCGGTGTGGAGCGCCAGTACCTGGCCAGGTC 64
QY 61 GACAGGGCGCGCGGCTTCCGTGCGCTCCATCGCCTCCAAAGGATGCGCCCATCATG 120
|||||
DB 65 GACAGGGCGCGCGGCTTCCGTGCGCTCCATCGCCTCCAAAGGATGCGCCCATCATG 124
QY 121 CTCGCGCTGCATGCATGATGCTGGACACTATGATGTGAACAAGAACTGATGTGCA 180
|||||
DB 125 CTCGCGCTGCATGCATGATGCTGGACACTATGATGTGAACAAGAACTGATGTGCA 184
QY 181 AATGTTCAATTAGATACGAGAGATACACCATGTTCAATGCTGGCTTAAATTT 240

DB 185 AATGTTCAATTAGATACGAGAGATACACCATGTTCAATGCTGGCTTAAATTT 244
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QY 241 GCTATGATCTCCTTGAGACCTTAATTAAGGAAAGCATCCAAAGATTATCATATGACAGCTT 300
|||||
DB 245 GCTATGATCTCCTTGAGACCTTAATTAAGGAAAGCATCCAAAGATTATCATATGACAGCTT 304
QY 301 CATCAGCTTCCGCGAGTATTCAGTTGAAGTCACCGGGGTCACACGTTAGTTTCATC 360
|||||
DB 305 CATCAGCTTCCGCGAGTATTCAGTTGAAGTCACCGGGGTCACACGTTAGTTTCATC 364
QY 361 CCTGGAAGACGTGATTCGTCACTTGTCCCGGTGAAGAGACGCTTCCTGATCTAAGAAA 420
|||||
DB 365 CCTGGAAGACGTGATTCGTCACTTGTCCCGGTGAAGAGACGCTTCCTGATCTAAGAAA 424
QY 421 GGTGACACCATCTTAAGGAGCATCTTTATCGAATGCGGTTAAAGACAAATATTTGA 480
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DB 425 GGTGACACCATCTTAAGGAGCATCTTTATCGAATGCGGTTAAAGACAAATATTTGA 484
QY 481 GCATCATCTGGGGGGGACAGCCTGGGAAAGCGCATCTGAAGAGTCTGGTTGACGGT 540
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DB 485 GCATCATCTGGGGGGGACAGCCTGGGAAAGCGCATCTGAAGAGTCTGGTTGACGGT 544
QY 541 GCATGACTCTGACCCCTCTGAAATTTGACAACTCATACTTCTTGAGCTACTGAAGGG 600
|||||
DB 545 GCATGACTCTGACCCCTCTGAAATTTGACAACTCATACTTCTTGAGCTACTGAAGGG 604
QY 601 GAATCTGAGGCTCTTCTGAAGCTCCCTACTGATTAAGGCACTTTGTGATATCTGAATTT 660
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DB 605 GAATCTGAGGCTCTTCTGAAGCTCCCTACTGATTAAGGCACTTTGTGATATCTGAATTT 664
QY 661 CG 662
||
DB 665 CG 666
RESULT 10
AV940735 677 bp mRNA linear EST 18-JAN-2002
LOCUS AV940735
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
CDNA clone ban29a06 5', mRNA sequence.
ACCESSION AV940735 GI:18236532
VERSION AV940735.1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 677)
AUTHORS Sato, K., Saitoh, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
FEATURES
source
1. 677
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="ban29a06"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 158 a 169 c 185 g 165 t
ORIGIN

Query Match 60.3%; Score 656.4; DB 9; Length 677;
 Best Local Similarity 99.8%; Pred. No. 5.8e-123;
 Matches 657; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CTTCTAGGTCGTCGCGGATGAGGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 60
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 20 CTTTGAAGGTCGTCGCGGATGAGGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 79
 |||||||
 61 GACAGGCGCGCGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 120
 |||||||
 80 GACAGGCGCGCGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 139
 |||||||
 121 CTCGCGCTGCGATGATGATGCTGGCAGCTATGATGTGAACACAGACTGTGTGTCGA 180
 |||||||
 140 CTCGCGCTGCGATGATGATGCTGGCAGCTATGATGTGAACACAGACTGTGTGTCGA 199
 |||||||
 181 AATGGTCAATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 |||||||
 200 AATGGTCAATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 259
 |||||||
 241 GCTATGATCTCCTGAGCTATTAAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 300
 |||||||
 260 GCTATGATCTCCTGAGCTATTAAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 319
 |||||||
 301 CATCAGCTTGGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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 320 CATCAGCTTGGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 379
 |||||||
 361 CCGTGAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 |||||||
 380 CCGTGAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 439
 |||||||
 421 GGTGACACCATCTAAGGAGATCTTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 |||||||
 440 GGTGACACCATCTAAGGAGATCTTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 499
 |||||||
 481 GCATGATCTGCGGAGGACAGACCTGCGGAAAGGCGCATCTGAAAGGCTGCGGTTGACGCT 540
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 500 GCATGATCTGCGGAGGACAGACCTGCGGAAAGGCGCATCTGAAAGGCTGCGGTTGACGCT 559
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 541 GCATGATCTGCGGAGGACAGACCTGCGGAAAGGCGCATCTGAAAGGCTGCGGTTGACGCT 600
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 560 GCATGATCTGCGGAGGACAGACCTGCGGAAAGGCGCATCTGAAAGGCTGCGGTTGACGCT 619
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 601 GAATCTGAGAGGCTCTGTAAGGCTCCCTAGTATGATGATGATGATGATGATGATGATGATGAT 658
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 620 GAATCTGAGAGGCTCTGTAAGGCTCCCTAGTATGATGATGATGATGATGATGATGATGATGAT 677
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RESULT 11
 LOCUS BF254606 863 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSMEF004H23f Hordeum vulgare seedling root EST library HVCNMA0007
 (Etiolated and unstressed) Hordeum vulgare cDNA clone
 HVSMEF004H23f, mRNA Sequence.
 ACCESSION BF254606
 VERSION BF254606.1 GI:11183711
 KEYWORDS EST.
 SOURCE Hordeum vulgare
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 863)
 Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Frisch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Panton
 , R.D., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex unstressed seedling root cDNA library
 Unpublished (2001)
 JOURNAL
 COMMENT
 Clemson University Genomics Institute

Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 436
 Seq primer: AATTAACCTCAGTAAAGG
 High quality sequence start: 10
 High quality sequence stop: 787.
 Location/Qualifiers
 1. 863
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEF004H23f"
 /clone_lib="Hordeum vulgare seedling root EST library
 HVCNMA0007 (Etiolated and unstressed)"
 /issue_type="Seedling root"
 /lab_host="TUC121"
 /note="Vector: lambdaZAP, Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under aseptic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedling roots were
 then harvested, total RNA was prepared, poly(A) RNA was
 purified, one primary unamplified cDNA library was made,
 and 1 million pfu were in vivo excised to give plasmid
 SK(-) cDNA phagemids. These steps were performed in the TU
 close laboratory at the University of California,
 Riverside (Choi, Close, Panton). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wang). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html)"

BASE COUNT 212 a 231 g 209 t 1 others
 ORIGIN

Query Match 58.7%; Score 639.2; DB 10; Length 863;
 Best Local Similarity 89.7%; Pred. No. 1.8e-119;
 Matches 733; Conservative 0; Mismatches 74; Indels 10; Gaps 4;

2 TTCTAGGTCGTCGCGGATGAGGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 61
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 51 TTCTAGGTCGTCGCGGATGAGGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 110
 |||||||
 62 ACAGGCGCGCGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 121
 |||||||
 111 ACAGGCGCGCGCGGCTCCGGTGTGACGCCAGTACCTGCGCCAGTGC 170
 |||||||
 122 TCCGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 181
 |||||||
 171 TCCGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 230
 |||||||
 182 AATGGTCAATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
 |||||||
 231 AATGGTCAATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 290
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 242 CATTGATCTCCTGAGCTATTAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
 |||||||
 291 CATTGATCTCCTGAGCTATTAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 350
 |||||||
 302 ATCAGCTTGGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
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Db 351 ATACGCTGCCGAGTAGTTGCAAGTCAACCGGGGTCACACCGTTGAGTTCATCC 410
 QY 362 CTGGAAGACGTGATGTCGATGTTGTCCCGGTGAAGACGCTTCTGATGTAAGAAG 421
 Db 411 CTGGAAGACGTGATGTCGATGTTGTCCCGGTGAAGACGCTTCTGATGTAAGAAG 470
 QY 422 GTGCACCAATCTAAGGACATCTTTATCGAATGGGGTTTAACAGCAAGAATATTGAG 481
 Db 471 GTGCACCAATCTAAGGACATCTTTATCGAATGGGGTTTAACAGCAAGAATATTGAG 530
 QY 482 CACTATCTGGGGGACACGCTGGGAAAGCGCATCTGAAGGCTGGGGTTGAGGAG 541
 Db 531 CACTATCTGGGGGACACGCTGGGAAAGCGCATCTGAAGGCTGGGGTTGAGGAG 590
 QY 542 CATGACGTGTCACCTCTGAATTTGACAACTCATCTTCTTGAGTACTGAAGGGG 601
 Db 591 CATGACGTGTCACCTCTGAATTTGACAACTCATCTTCTTGAGTACTGAAGGGG 650
 QY 602 AATCTAGGCTCTTGAAAGCTCCCTAGTGAATAGGCATTTGATGATCTGAATTC 661
 Db 651 AATCTAGGCTCTTGAAAGCTCCCTAGTGAATAGGCATTTGATGATCTGAATTC 709
 QY 662 GACGCTAGGAGCTTTAGCAAGGATGAGATGTTTCTTCAAGGACTACGCTGAAT 721
 Db 710 AGCCTTGGGGCTTTTGAAGAGAGAGATG----TTTGTATAGGGCTACCTG-- 762
 QY 722 CACACAAAAAATTCTGAACTGGCTTCACACGAGAGAGAGAGAGAGATCTACAA 781
 Db 763 TACACAAAAAATTCTGAACTGGCTTCACAA--GAGGGGTTGGCACCCTTTAGCAA 820
 QY 782 AATCAGATGTTCACTGCTGTTTGTACTTGCACAGAG 818
 Db 821 AAAAAATGTTAGACTGCTCTTGACCTGACCAAAAG 857

RESULT 12

AV938146

LOCUS

AV938146 654 bp mRNA linear EST 18-JAN-2002
 AV938146 K. Sato unpublished cDNA library, strain H602 adult,
 heading stage top three leaves Hordeum vulgare subsp. spontaneum
 cDNA clone bahl6f21 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .654

/organism="Hordeum vulgare subsp. spontaneum"

/strain="H602"

/db_xref="taxon:77009"

/clone="bahl6f21"

/clone.lib="K. Sato unpublished cDNA library, strain H602

adult, heading stage top three leaves"

/tissue.type="top three leaves"

/dev.stage="adult, heading stage"

BASE COUNT

152 a 166 c 178 g 158 t

Query Match 58.1%; Score 632.4; DB 9; Length 654;
 Best Local Similarity 99.8%; Pred. No. 4.2e-118;
 Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTTATGGGTCGTCGCGATGAGGGGCTCGGTGGGAGCCGAGTACTGGGCCAGGTC 60
 Db 21 CTTTATGGGTCGTCGCGATGAGGGGCTCGGTGGGAGCCGAGTACTGGGCCAGGTC 80
 QY 61 GACAGGGCGCGCGCGCTTCGCTTCATCGCTCCCAAGAGATGCGCCCATCATG 120
 Db 81 GACAGGGCGCGCGCGCTTCGCTTCATCGCTCCCAAGAGATGCGCCCATCATG 140
 QY 121 CTCGCGCTCGCATGCGCATGATCGTGGACCTATGATGTGAACAAAGAACTGGTGTGA 180
 Db 141 CTCGCGCTCGCATGCGCATGATGCTGGACCTATGATGTGAACAAAGAACTGGTGTGA 200
 QY 181 AATGTTCAATTAGATACAGAGAGAGTACACCATGTTCAAAAGTCTGTTAAATTT 240
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 QY 241 GCTATGATCTGCTTGAGGCTATTAAAGCAAGCATCCAAAGATTACATATGACAGCTT 300
 Db 261 GCTATGATCTGCTTGAGGCTATTAAAGCAAGCATCCAAAGATTACATATGACAGCTT 320
 QY 301 CATCAGCTTCCGAGATGATGTCAGTTGAAGTACCGGGGGTCCAAACGTTGATTCATC 360
 Db 321 CATCAGCTTCCGAGATGATGTCAGTTGAAGTACCGGGGGTCCAAACGTTGATTCATC 380
 QY 361 CCTGGAGACGTGATTCGTCATTTGTCCCGGTGAAGAGAGCGCTTCTTATGTAAGAA 420
 Db 381 CCTGGAGACGTGATTCGTCATTTGTCCCGGTGAAGAGAGCGCTTCTTATGTAAGAA 440
 QY 421 GGTGCACCAATCTAAGGAGACATCTTTATCGAATGGGGTTAAACAGCAAGAATATTGA 480
 Db 441 GGTGCACCAATCTAAGGAGACATCTTTATCGAATGGGGTTAAACAGCAAGAATATTGA 500
 QY 481 GCATATCTGGGGGACAGCCTGGGAAAGCGCATCTGAAAGGTGTTGTCAGCT 540
 Db 501 GCATATCTGGGGGACAGCCTGGGAAAGCGCATCTGAAAGGTGTTGTCAGCT 560
 QY 541 GCATGACCTGTCGACCTGTAATTTGACAACTCATCTTCTTGAGTACTGAAGGGG 600
 Db 561 GCATGACCTGTCGACCTGTAATTTGACAACTCATCTTCTTGAGTACTGAAGGGG 620
 QY 601 GAATCGAGGCTCTTCTGAAAGCTCCCTACTGATA 634
 Db 621 GAATCGAGGCTCTTCTGAAAGCTCCCTACTGATA 654

RESULT 13

AV934694/c

LOCUS

AV934694 652 bp mRNA linear EST 18-JAN-2002
 AV934694 K. Sato unpublished cDNA library, cv. Hazuna Nijo adult,
 heading stage top three leaves Hordeum vulgare subsp. vulgare
 cDNA clone baalle16 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. (bases 1 to 652)

/organism="Hordeum vulgare subsp. vulgare"

/strain="H602"

/db_xref="taxon:77009"

/clone="bahl6f21"

/clone.lib="K. Sato unpublished cDNA library, strain H602

adult, heading stage top three leaves"

/tissue.type="top three leaves"

/dev.stage="adult, heading stage"

BASE COUNT

152 a 166 c 178 g 158 t

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Db 604 GAATCTGAGGCTCTCTGAGACTCCCT 630

RESULT 15

AV909151

LOCUS

DEFINITION

AV909151 672 bp mRNA linear EST 18-JAN-2002

AV909151 K. Sato unpublished cDNA library, cv. Akashinriki

vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone

baak1m21 5', mRNA sequence.

AV909151

AV909151.1 GI:18204700

EST.

Hordeum vulgare subsp. vulgare.

Hordeum vulgare subsp. vulgare.

Eukaryota: Viridiplantae: Streptophyta: Tracheophyta:

Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Poideae

; Triticeae; Hordeum.

1 (bases 1 to 672)

Sato, K., Saitoh, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasi Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1. 672

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Akashinriki"

/db_xref="taxon:112509"

/clone="baak1m21"

/clone_1lb="K. Sato unpublished cDNA library, cv.

Akashinriki vegetative stage leaves"

/tissue_type="leaves"

/dev_stage="vegetative stage"

BASE COUNT 153 a 178 c 184 g 157 t

ORIGIN

Query Match 57.2%; Score 623.4; DB 9; Length 672;

Best Local Similarity 99.8%; Pred. No. 2.8e-116;

Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCTAGGGTCCTCCGCGATGGGGCTCCGGTGTGGAGCGCGAGTACTGCGCCAGGTC 60

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Db 48 CTCTAGGGTCCTCCGCGATGGGGCTCCGGTGTGGAGCGCGAGTACTGCGCCAGGTC 107

QY 61 GACAGGGCGCGCGCGCTTCCTGCTCATCGCTCCCAAGGATGCGCCCATCATG 120

|||||

Db 108 GACAGGGCGCGCGCGCTTCCTGCTCATCGCTCCCAAGGATGCGCCCATCATG 167

QY 121 CTCGCCCTCGCATGCGATGCTGGCACCTATGATGTGAACACAGAACTGGTGTGCA 180

|||||

Db 168 CTCGCCCTCGCATGCGATGCTGGCACCTATGATGTGAACACAGAACTGGTGTGCA 227

QY 181 AATGGTTCAATTAGTACAGAGAGAGTACACCATGTTCAATGCTGGCTTAATAATT 240

|||||

Db 228 AATGGTTCAATTAGTACAGAGAGAGTACACCATGTTCAATGCTGGCTTAATAATT 287

QY 241 GCTATTGATCTCTTGAAGCTTAAAGGAAAGCATCAAAAGTTACATATGAGACCTT 300

|||||

Db 288 GCTATTGATCTCTTGAAGCTTAAAGGAAAGCATCAAAAGTTACATATGAGACCTT 347

QY 301 CATCAGCTTGCAGGAGTACTGTCAGTTGAAGTACCGGGGGTCCAAACGTTGATTCATC 360

|||||

Db 348 CATCAGCTTGCAGGAGTACTGTCAGTTGAAGTACCGGGGGTCCAAACGTTGATTCATC 407

QY 361 CCGGAAGAGTATGTCAGTTGTGTCCTCCCGGAAGAGAGCGCTTCCATGCTAGAGAA 420

|||||

Db 408 CCGGAAGAGTATGTCAGTTGTGTCCTCCCGGAAGAGAGCGCTTCCATGCTAGAGAA 467

QY 421 GGTCACACATCTTAAGGAGACATCTTTATCGAATGGGGTTAAACAGACAATATTCTA 480

|||||

Db 468 GGTGCACACATCTTAAGGAGACATCTTTATCGAATGGGGTTAAACAGACAATATTCTA 527

QY 481 GCATATCTGGGGGCGACAGCCTGGGAAAGCCCATCTGAAAGGCTGTGGTTGACGCT 540

|||||

Db 528 GCATATCTGGGGGCGACAGCCTGGGAAAGCCCATCTGAAAGGCTGTGGTTGACGCT 587

QY 541 GCATGACCTCGACCCCTCTGAAATTTGACAACTCATTTCTTGTAGCTACTGAAAGGG 600

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Db 588 GCATGACCTCGACCCCTCTGAAATTTGACAACTCATTTCTTGTAGCTACTGAAAGGG 647

QY 601 GAATCTGAGGCTCTTCTGAAAGCTCC 625

|||||

Db 648 GAATCTGAGGCTCTTCTGAAAGCTCC 672

Search completed: October 25, 2002, 17:29:25

Job time : 1727 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 16:18:41 ; Search time 50 Seconds

(without alignments)
5349,898 Million cell updates/sec

Title: US-09-870-501-2

Perfect score: 1089

Sequence: 1 cttcagggtcgtccgcgat.....gaataaaaaaaaaaaaaa 1089

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCrus.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303.6	27.9	1229	2 US-08-975-316-85	Sequence 85, Appl
2	174.2	16.0	557	1 US-08-266-451B-17	Sequence 17, Appl
3	174.2	16.0	557	2 US-08-746-725-17	Sequence 17, Appl
4	106.2	9.8	471	2 US-08-975-316-43	Sequence 43, Appl
5	38	3.5	1836	1 US-07-929-580B-1	Sequence 1, Appl
6	37.8	3.5	1167	2 US-08-671-320-16	Sequence 16, Appl
7	37.8	3.5	1167	2 US-08-868-577-16	Sequence 16, Appl
8	36.4	3.3	2268	3 US-08-753-007A-31	Sequence 31, Appl
9	36.4	3.3	2268	3 US-09-396-496-31	Sequence 31, Appl
10	35	3.2	1048	4 US-09-227-357-145	Sequence 145, App
11	34.8	3.2	1939	6 5198542-3	Patent No. 5198542
12	34.8	3.2	17041	1 US-08-076-011-1	Sequence 1, Appl
13	34.6	3.2	1191	2 US-08-671-320-14	Sequence 14, Appl
14	34.6	3.2	1191	2 US-08-868-577-14	Sequence 14, Appl
15	34.6	3.2	2455	4 US-09-103-429A-1	Sequence 1, Appl
16	34.6	3.2	2821	4 US-09-103-429A-2	Sequence 2, Appl
17	34.2	3.1	485	2 US-08-997-080-41	Sequence 41, Appl
18	34.2	3.1	485	2 US-08-997-080-41	Sequence 41, Appl
19	34.2	3.1	485	2 US-08-997-362-41	Sequence 41, Appl
20	34.2	3.1	485	2 US-08-997-362-106	Sequence 106, App
21	34.2	3.1	485	3 US-08-873-970-41	Sequence 41, Appl
22	34.2	3.1	485	3 US-08-873-970-106	Sequence 106, App
23	34.2	3.1	485	4 US-09-095-855-41	Sequence 41, Appl
24	34.2	3.1	485	4 US-09-095-855-106	Sequence 106, App
25	34.2	3.1	485	4 US-08-705-347A-41	Sequence 41, Appl
26	34.2	3.1	485	4 US-09-324-542-41	Sequence 41, Appl
27	34.2	3.1	485	4 US-09-324-542-106	Sequence 106, App

28	34.2	3.1	1217	4 US-09-277-716-17	Sequence 17, Appl
29	33.8	3.1	1211	2 US-08-997-060-40	Sequence 40, Appl
30	33.8	3.1	1211	2 US-08-997-362-40	Sequence 40, Appl
31	33.8	3.1	1211	3 US-08-873-970-40	Sequence 40, Appl
32	33.8	3.1	1211	4 US-09-095-855-40	Sequence 40, Appl
33	33.8	3.1	1211	4 US-08-705-347A-40	Sequence 40, Appl
34	33.8	3.1	1211	4 US-09-324-542-40	Sequence 40, Appl
35	33.8	3.1	6060	5 PCT-US96-09430-7	Sequence 7, Appl
36	33.6	3.1	2220	4 US-08-765-907A-14	Sequence 14, Appl
37	33.6	3.1	3147	2 US-08-781-802-7	Sequence 7, Appl
38	33.6	3.1	3147	4 US-09-058-260-7	Sequence 7, Appl
39	33.6	3.1	3147	4 US-08-765-907A-6	Sequence 6, Appl
40	33.6	3.1	4496	4 US-08-293-728-1	Sequence 1, Appl
41	33.2	3.0	3498	3 US-09-421-868-1	Sequence 1, Appl
42	33.2	3.0	8920	2 US-08-446-855A-1	Sequence 1, Appl
43	33.2	3.0	8920	4 US-09-150-741-1	Sequence 1, Appl
44	33.2	3.0	8920	2 US-08-107-676-26	Sequence 26, Appl
45	33	3.0	1178	2 US-08-107-676-26	Sequence 26, Appl

ALIGNMENTS

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RESULT 1
US-08-975-316-85
; Sequence 85, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-85
;
; Query Match 27.9%; Score 303.6; DB 2; Length 1229;
; Best Local Similarity 63.4%; Pred. No. 2.1e+83;
; Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;
; GCATGCGGCTCCGGTGTGACCGCGAGTACTGCGCCAGTGCAGAGGCGCGCCG 75
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Db 222 GTGAAGGGCTTATCCACCCCTTAAGCGAGAGTACAAAGCTGCTCCATTGACAAATCCAAAGG 281
QY 76 GCGTTCGCGTCCCTATCCCTCCACAGGAGTGGCCCCCATCATGCTCCCTCGCATG 135
Db 282 AAGGTCGAGGCTCTATTCAGAGAAAGAACTGTGGCCGCAATGATGTTGCAATCGCATG 341
QY 136 CATGATGCTGGCACTATATATGTAACACAAAGACTGTGGTGCMAATGGTTCAATAGA 195
Db 342 CACAGCGGCTGACTTACATGTCACAGACCAAGACCAGGAGGCGCTTCGGGAGATGAGA 401
QY 196 TACGAGGAAGATACACCAGTGTTCAAATGCGGCTTAAATTTGCTATATGATTCCTT 255
Db 402 TATGGGGCCGACTTGGCCACAGGTGCTACAGTGTCTGACATCGAGATTAGGCTCTG 461
QY 256 GAGCCTATTAAACGAGACATCCAAAGATTACATATGACAGACCTTCATCATCTTCCCGGA 315
Db 462 GAGCAATCAAGAGAACAGTTCGCCAATATCACCCTATGCTGACCTTTATCGATGGCGGT 521
QY 316 GTAGTTGCAATTGAAGTCAACCGGGGGTCCAAACCGTTGAGTTCAATCCCTGGAAGACTGAT 375
Db 522 GTGGTGGCTGTTGAAGTGAACCGGGGACCTGACATTCCTCCATCTCGGAAGAGAAC 581
QY 376 TCGTAGTTTGTCCCGTAAGAGCGCTTCTGATGCTAAGAAAGTGCACACATCTA 435
Db 582 AAGCCTGAGCCTCCAGAAAGAGCGCTTCTGATGCTACAAAGAGACCTGATCATCTG 641
QY 436 AAGGACATCTTTTATCGAATGGGCTTACAGACAAAGATATTGATGACATCTTGGGGG 495
Db 642 AAGGATGTTTGTGTCACATGGGGTTGAATGAATGAATGTTGGCCTGTGTGGGCC 701
QY 496 CACAGCCTGGGAAAGCGCATCTCAAGAGTCTGGGTTGACGGTGCATGAGACTCGTAC 555
Db 702 CACACCTTGGGAGATGACCAAGAGAGATCTGGTTTGAAGACCATGAGACCTCTAAC 761
QY 556 CCTGGAATTTGACAACTCATCTTCTTGAAGTCTAGGAGGGAATGAGGGGCTT 615
Db 762 CCCCTTATCTTGAACACTTACTTACAGAGCTGTGACTGAGAGAGAAAGAGGCTG 821
QY 616 CTGAAGCTCCCTAGTGAATGAGCATTTGATGATCTGGAATTTGACAGCTATGTTGAG 675
Db 822 CTTCAGTTCCTGATGATGAGCAGCTGTGCTGATCTAGTTTTCAGATTTATGTTACG 881
QY 676 CTTTGAAGAGATGAGATGTTTCTTCAAGACTAGCTGAATACACAAAAACTT 735
Db 882 AAGTATGACAGAGCAAGAACGCTTCTTCTGCTGATGCGGAACCTCACTGAAGCTT 941
QY 736 TCTGAACCTGGCTT 749
Db 942 TCTGAACCTGGCTT 955

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RESULT 2

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US-08-266-451B-17
; Sequence 17, Application US/08266451B
; Patent No. 5623054
; GENERAL INFORMATION:
; APPLICANT: Zhang et al.
; TITLE OF INVENTION: CRUCIFER AFT PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,451B
; FILING DATE: 23-June-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Iech, Karen F.
; REGISTRATION NUMBER: 35,238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ. ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-266-451B-17

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Query Match 16.0%; Score 174.2; DB 1; Length 557;

Best local Similarity 68.5%; Pred. No. 8e-44; Matches 261; Conservative 0; Mismatches 108; Indels 12; Gaps 1;

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QY 514 CATCTGAAAGTCTGCGTTGACGCTGATGACTGTCGACCTCTGAAATTTGACAAC 573
Db 2 CACCCAGAGAGAGTCCAGCTTTGATGACCATGAGCCCAAGACCCGCTGAAGTTGACAAC 61
QY 574 TCATCTTCTTGTAGTACTGAGGAGGAAATCGAGGCTCTGAGCTCCCTCTGAT 633
Db 62 TCCTACTTCTGGAATGCTGAAAGAGAAATCAGAGGCTTTGTAATTTCAACTGAC 121
QY 634 AAGCATTTGTTGATGATCTGAAATTTGACGCTATGTGAGCTTATGCAAGATGAG 693
Db 122 AAGACCTTATGGAAGACCCGAGTTCGCGTGTGAGCTTATGCAAGATGAA 181
QY 694 GATGTTTCTCAAGACATGCTGAAATCAGCAAAACTTTGTAATTTGGCTTACA 753
Db 182 GATGATTTCTCAAGACATGCGGGAATGACAAAGAACTCTGAGCTGTTGTTCAAC 241
QY 754 CCAAGAGAGAGTGGCCAGCATCTACAAATCAGATGTTTCAACAGCTGTTACTTCA 813
Db 242 CCA-----AACCTCAGAGAGCAAGCAAGTTGACAGACAGCATTTTGCA 289
QY 814 CAGATGCAAGTGGGTTAGCAGTTGCTGCACTGATGATGCGGGCTACCTGTACGAA 873
Db 290 CAGAGTGGCTTGGGGTTGACAGTTGCTGCGGTTGTGCAATTTGATCTTTACGAG 349
QY 874 GCTTCAAGAGAGCAAGTAA 894
Db 350 ATTGGGAAGAGATGAATGA 370

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RESULT 3

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US-08-748-725-17
; Sequence 17, Application US/08748725
; Patent No. 5859346
; GENERAL INFORMATION:
; APPLICANT: Zhang et al.
; TITLE OF INVENTION: CRUCIFER AFT PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)

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RESULT 7
 US-08-868-577-16
 ; Sequence 16, Application US/08868577
 ; Patent No. 5866695
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Vierling Jr., Richard A
 ; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
 ; TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
 ; NUMBER OF SEQUENCES: 19
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
 ; STREET: 555 13th Street NW, Suite 701 East
 ; CITY: Washington
 ; STATE: DC
 ;
 ; COUNTRY: USA
 ;
 ; ZIP: 20004
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 6.1
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/868,577
 ; FILING DATE: 04-JUN-1997
 ;
 ; CLASSIFICATION: 536
 ;
 ; ATTORNEY/AGENT INFORMATION:

```

NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
TELEFAX: 402-333-1510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..38
FEATURE:
NAME/KEY: CDS
LOCATION: 39..977
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 978..1167
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 39..101
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 102..977

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RESULT 8
 US-08-753-007A-31/C
 Sequence 31, Application US/08753007A
 Patent No. 6074841
 GENERAL INFORMATION:
 APPLICANT: Gearing, David P.
 APPLICANT: Busfield, Samantha J.
 TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
 TITLE OF INVENTION: AND USES THEREFOR
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/753,007A
 FILING DATE: 19-NOV-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/699,591
 FILING DATE: 19-AUG-1996
 ATTORNEY/AGENT INFORMATION:

```

1 NAME: Fasse, J. Peter
2 REGISTRATION NUMBER: 32,983
3 REFERENCE/DOCKET NUMBER: 07334/022001
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 617-542-5070
6 TELEFAX: 617-542-8906
7
8 TELEX:
9
10 INFORMATION FOR SEQ ID NO: 31:
11
12 SEQUENCE CHARACTERISTICS:
13
14 LENGTH: 2268 base pairs
15
16 TYPE: nucleic acid
17
18 STRANDEDNESS: single
19
20 TOPOLOGY: linear
21
22 MOLECULE TYPE: cDNA
23
24 FEATURE:
25
26 NAME/KEY: Coding Sequence
27 LOCATION: 69...2009
28
29 OTHER INFORMATION:
30
31 US-08-753-007A-31

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	Matches	70	Conservative	0	Mismatches	56
					Indels	0
					Gaps	0
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Dd	1815 CGTCGCGCTCGTCGCGCGTGTGTGTCCGACAGCCGAGAGGTGAGCGCGCCGACCGCGTCC	1756				
QY	71 GCGCGCCTTCCGTCCTCATCGCCTCCMAAGGATGCGCCCCCATCATGCTCGGCTTG	130				
Dd	1755 TCAGCGACAGGAGAGTCCCTCCGCCGCCCGTGGCGCTGGCGCCGACCGCGTTGAGAGCGG	1696				
QY	131 CATGCG	136				
Dd	1695 AGCGGC	1690				

RESULT 9
US-09-398-496-31/c
Sequence 31, Application US/09398496
Patent No. 6133423
GENERAL INFORMATION:
APPLICANT: Geating, David P.
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,496
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/753,007
FILING DATE: 19-NOV-1996
APPLICATION NUMBER: 08/699,591
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Passe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334/022001
TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 69...2009
; OTHER INFORMATION:
;
US-09-398-496-31

Query Match          3.3%; Score 36.4; DB 3; Length 2268;
Best Local Similarity 55.6%; Pred.No.0.49;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Db 1815 CGTCGCGATGAGCGGCTCGGTGAGAGCGCCGAGTACCTCGCGCCAGTCAGACAGGCGC 1756
    |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 71 GCGCGCGCTTCGCGGCTCGGTGAGAGCGCCGAGTACCTCGCGCCAGTCAGACAGGCGC 130
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Db 1755 TCACGCGACGAGTCCCTCGCGCCGCTGCGCGCTGCGCGCCAGTCAGACAGGCGC 1696
    |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 131 CATGAC 136
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Db 1695 AGCGGC 1690

RESULT 10
US-09-227-357-145
; Sequence 145, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; EARLIER FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08

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; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (79)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (625)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-227-357-145

Query Match          3.2%; Score 35; DB 4; Length 1048;
Best Local Similarity 55.3%; Pred.No.0.79;
Matches 68; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 967 CCAAGTGAATTAACAGACTCTAGTGAACCAACAGTAGTCTCAAAATATTTC 1026

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[illegible]

RESULT 11
 5198542-3/c
 ; Patent No. 5198542
 ; APPLICANT: ONDA, HARUO; ARIMURA, AKIRA; KIMURA, CHI HARU
 ; KITADA, CHERO
 ; TITLE OF INVENTION: DNA ENCODING A PITUITARY ADENYLATE CYCLASE
 ; ACTIVATING PROTEIN AND USE THEREOF
 ; NUMBER OF SEQUENCES: 16
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/540,105
 ; FILING DATE: 10-JUN-1990
 ; SEQ ID NO.: 3:
 ; LENGTH: 1939
 5198542-3

Query Match	3.2%	Score	34.8	DB	6	Length	1939
Best Local Similarity	52.8%	Pred.	No. 1.4				
Matches	75	Conservative	0	Mismatches	67	Indels	0
						Gaps	0

Qy	925	TTATTAGTAAATCAAGTATTTATTTCAAAAAAATAGTCCCAAGTCGAATTAACGA	984
Db	890	TGATTGCTACTTTTCATATTTATTTATTTAAACATTAACGCTGGCGGCAATTTTCA	831
Qy	985	ACCTAGTGAAGAAACACAGAGTGTCTCAAAATATTCATCACTCTGAGGACATC	104
Db	830	TCCTCTGACAGCGTTTGTAAGCACTCTCTCTATCTTATATATATATATATATATA	771
Qy	1045	TCCTTCATATATATACATCAATA	1066
Db	770	TTCTTTATATATATTTATATA	749

RESULT 12
 US-08-076-011-1/c
 : Sequence 1, Application US/08076011
 : Patent No. 5521069
 : GENERAL INFORMATION:
 : APPLICANT: ONDA, Haruo
 : APPLICANT: KIMURA, Chiharu
 : APPLICANT: OKHIBO, Shoichi
 : TITLE OF INVENTION: NOVEL DNA AND USE THEREOF
 : NUMBER OF SEQUENCES: 3
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN,
 : ADDRESSEE: ROBERTS & CUSHMAN
 : STREET: 130 Water Street
 : City: Boston
 : STATE: Massachusetts
 : COUNTRY: US
 : Zip: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/076,011
 : FILING DATE: 11-JUN-1993
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/047,246

FILING DATE: 13-APR-1993
 NAME:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/741,676
 FILING DATE: 07-AUG-1991
 NAME:
 ATTORNEY/AGENT INFORMATION:
 NAME: RESNICK, DAVID S
 REGISTRATION NUMBER: 34235
 REFERENCE/DOCKET NUMBER: 41155-CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)523-3400
 TELEFAX: (617)523-6440
 TELEX: 200291 STRE UR
 INFORMATION FOR SEO ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17041 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(7540..7650, 9814..9945, 10421..10519,
 11602..11787)
 US-08-076-011-1

Query Match	3.2%	Score	34.8	DB	1	Length	17041
Best Local Similarity	52.8%	Pred.	No. 5.8				
Matches	75	Conservative	0	Mismatches	67	Indels	0
						Gaps	0

QY	985	ACGCTGATGATGAAACCAACAGAGACGTCAAAATATTCATCATCTTGAGGACATC	1044
Db	12089	TCCCTGGCGACGGTTTGATGGAACCTTCCTCATACCTTATATATATATATATATATA	12030
QY	1045	TCCCTCATATATATACATCATATA	1066
Db	12029	TTCTTATATATATATATATATAATA	12008
QY	925	TTTATTAGTAAAGATCAACATATATATTTCTTAAAAAAATTAAGCCCAATGCAAAATACAG	984
Db	12149	TGAATGCGCACTTTCTTATATTTATTTTAAAAAATATAAGATCGGGCAATTTTCAA	12090

RESULT 13
 US-08-671-320-14
 Sequence 14, Application US/08671320
 Patent No. 5840558
 GENERAL INFORMATION:
 APPLICANT: VIERLING JR, RICHARD A
 TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
 ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: 1125 SO. 103RD STREET
 STREET, SUITE 330
 CITY: OMAHA
 STATE: NE
 COUNTRY: US
 ZIP: 68124-1076
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/671,320
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: JONDLE, ROBERT J.
 REGISTRATION NUMBER: 33,915
 REFERENCE/DOCKET NUMBER: 1227-001

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
TELEFAX: 402-398-9005
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..59
FEATURE:
NAME/KEY: CDS
LOCATION: 60..998
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 999..1191
FEATURE:
NAME/KEY: s1g_peptide
LOCATION: 60..122
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 123..998
US-08-671-320-14

Query Match
Best Local Similarity 64.2%; Score 34.6; DB 2; Length 1191;
Matches 52; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 426 ACCACATCTAAGGACATCTTTATCGAATGGGGTTAACAGACAAAGATATGTGACACT 485
DB 551 ATCACACTGCGCGCAAGATTCTCTCAAGAGAGACTGTGAGGGAAGACCTGTACTCT 610
OY 486 ATCTGGGGGCGACACGCTGGG 506
DB 611 GTCAGGGGGCGACACTTTGGG 631

RESULT 14
US-08-868-577-14
; Sequence 14, Application US/08868577
; Patent No. 5868695
; GENERAL INFORMATION:
; APPLICANT: Vierling Jr., Richard A
; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Flagg, Ernst & Kurz
; STREET: 555 13th Street NW, Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/868,577
; FILING DATE: 04-JUN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jomale, Robert J.
; REGISTRATION NUMBER: 33,915
; REFERENCE/DOCKET NUMBER: N1227-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 402-333-1550
; TELEFAX: 402-333-1510
; INFORMATION FOR SEQ ID NO: 14:
```

```
SEQUENCE CHARACTERISTICS:
LENGTH: 1191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 60..998
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..59
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 999..1191
FEATURE:
NAME/KEY: s1g_peptide
LOCATION: 60..122
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 123..998
US-08-868-577-14

Query Match
Best Local Similarity 64.2%; Score 34.6; DB 2; Length 1191;
Matches 52; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 426 ACCACATCTAAGGACATCTTTATCGAATGGGGTTAACAGACAAAGATATGTGACACT 485
DB 551 ATCACACTGCGCGCAAGATTCTCTCAAGAGAGACTGTGAGGGAAGACCTGTACTCT 610
OY 486 ATCTGGGGGCGACACGCTGGG 506
DB 611 GTCAGGGGGCGACACTTTGGG 631

RESULT 15
US-09-103-429A-1/c
; Sequence 1, Application US/09103429A
; Patent No. 6187558
; GENERAL INFORMATION:
; APPLICANT: Granados, Robert R
; TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
; STREET: 118 No. 6187558th Tloga
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,429A
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: BTI-39
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (607) 256-2000
; TELEFAX: (607) 256-3628
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2455 base pairs
; TYPE: nucleic acid
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```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Trichoplusia ni
; TISSUE TYPE: peritrophic Membrane
; IMMEDIATE SOURCE:
; CLONE: IM14
; US-09-103-429A-1

```

```

Query Match          3.2%; Score 34.6; DB 4; Length 2455;
Best Local Similarity 55.4%; Pred. No. 1.8;
Matches 67; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

```

```

Qy 741 ACTTGCTTCACACACGAGAGTGGCCACGATCTACAAATCAGATGTTCAACTGC 800
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 781 ATTGGGCAACAGTTCACAGATCGGGGCCAGACTGGGCTGAAGTGGGTGCAGAACACC 722
Qy 801 TGTGTACTTGCACAGAGTGCAGTGGGGGTAGAGTTGCTGCAGCTGTATTCGCGGG 860
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 721 TGGGGTAGTTCAGCGGGGGGTGTCTCCGCCAGAGGGTAGTTGCCGCCGGGGTAGTTCGCGC 662
Qy 861 C 861
   |
Db 661 C 661

```

Search completed: October 25, 2002, 17:30:34
 Job time : 61 secs

•
•
•
•

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 18 Seconds

(without alignments)
1553.444 Million cell updates/sec

Title: US-09-870-501-1

Perfect score: 1498
Sequence: 1 MAAPVDAEYLKQVDRARRA.....AVAAVYIAGLYEASRKS 291

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	82.8	288	2	T09845 L-ascorbate peroxi
2	1183	79.0	287	2	S71279 L-ascorbate peroxi
3	934.5	62.4	279	2	T04707 L-ascorbate peroxi
4	834.5	55.7	250	2	T07056 L-ascorbate peroxi
5	824.5	55.0	250	2	S68465 L-ascorbate peroxi
6	824.5	55.0	250	2	S49914 L-ascorbate peroxi
7	824	55.0	249	2	T10189 L-ascorbate peroxi
8	821.5	54.8	250	2	T03595 L-ascorbate peroxi
9	819.5	54.7	250	2	T09125 L-ascorbate peroxi
10	819.5	54.7	250	2	J60232 L-ascorbate peroxi
11	818.5	54.6	250	2	D86214 L-ascorbate peroxi
12	818.5	54.6	263	2	S20866 L-ascorbate peroxi
13	815.5	54.4	250	2	S43157 L-ascorbate peroxi
14	802.5	53.6	250	2	A45116 L-ascorbate peroxi
15	775.5	51.8	260	2	T12389 L-ascorbate peroxi
16	774.5	51.7	245	2	T12334 L-ascorbate peroxi
17	752.5	50.2	250	2	T08071 L-ascorbate peroxi
18	746.5	49.8	254	2	T12338 L-ascorbate peroxi
19	714.5	47.8	309	2	S66265 L-ascorbate peroxi
20	666	44.5	421	2	S71331 L-ascorbate peroxi
21	653	43.6	430	2	T12282 L-ascorbate peroxi
22	644.5	43.0	421	2	T10190 L-ascorbate peroxi
23	640.5	42.8	426	2	C96804 L-ascorbate peroxi
24	631.5	42.2	372	2	T14193 L-ascorbate peroxi
25	598	39.9	327	2	T08103 L-ascorbate peroxi
26	457	30.5	361	1	OPBYC cytochrome-c perox
27	317	21.2	735	4	J50520 catalase (EC 1.11.
28	317	21.2	751	4	T43873 catalase (EC 1.11.
29	317	21.2	751	4	T43874 catalase (EC 1.11.

30	317	21.2	751	4	T43878 catalase (EC 1.11.
31	317	21.2	751	4	T43880 catalase (EC 1.11.
32	317	21.2	751	4	T43881 catalase (EC 1.11.
33	317	21.2	752	4	T43877 catalase (EC 1.11.
34	317	21.2	753	4	T43882 catalase (EC 1.11.
35	309.5	20.7	735	2	B83763 catalase (EC 1.11.
36	294.5	19.7	724	2	B82186 catalase (EC 1.11.
37	294	19.6	737	2	AC0403 catalase (EC 1.11.
38	289.5	19.3	723	2	AF3127 catalase (EC 1.11.
39	289.5	19.3	731	2	C98160 catalase (EC 1.11.
40	280.5	18.7	731	2	T44846 catalase (EC 1.11.
41	277	18.5	736	2	T00313 catalase (EC 1.11.
42	276.5	18.5	736	2	T00313 catalase (EC 1.11.
43	266	17.8	754	2	S75113 catalase (EC 1.11.
44	265	17.7	741	2	A69529 catalase (EC 1.11.
45	261	17.4	166	2	T05342 L-ascorbate peroxi

ALIGNMENTS

```
RESULT 1
T09845
L-ascorbate peroxidase (EC 1.11.1.11), glyoxysomal - upland cotton
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Apr-2000
C:Accession: T09845
R:Bunkelmann, J.; Trelease, R.N.
submitted to the EMBL Data Library, September 1995
A:Description: Ascorbate peroxidase: A prominent membrane protein in oilseed glyoxys
A:Reference number: Z16882
A:Accession: T09845
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-288 <BN>
A:Cross-references: EMBL:U37060; NID:g1019945; P1D:g1019946
A:Experimental source: cultivar Deltapine 62
C:Function:
A:Description: catalyzes peroxidation of ascorbate to dehydroascorbate
C:Superfamily: cytochrome-c peroxidase
C:Keywords: chromoprotein; glyoxysome; heme; iron; metalloprotein; oxidoreductase
F:40/Active site: His (distal ligand) #status predicted
F:160/Binding site: Heme iron (His) (proximal axial ligand) #status predicted
F:176/205/Active site: Tyr, Asp #status predicted

Query Match      82.8%  Score 1240.5:  DB 2:  Length 288;
Best Local Similarity 80.4%:  Pred. No. 3e-95;
Matches 234;  Conservative 26;  Mismatches 28;  Indels 3;  Gaps 1;

QY  1  MAAPVDAEYLKQVDRARRAPRALIASKGCAPIMRLAMHDAGTYDVNTRTGANGSIRY  60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  1  MAAPVDAEYLKQVDRARRAPRALIASKGCAPIMRLAMHDAGTYDVNTRTGANGSIRN  60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  61  EEEYHGSNAGIKIAIDLEPKAKHPKITTYADLHQLAGVAAYEVETGGPVEFFIGRDS  120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  61  EEEYHGSNAGIKIAIDLEPKAKHPKITTYADLHQLAGVAAYEVETGGPVEFFIGRDS  120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  121  SVCPEGRPLDPAKKAAPHLRDFYRNGLTDRDITVALSGSHSGKHAHPRSRSGDGAWTDP  180
    ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
DB  121  NICEPEGRPLDPAKKAAPHLRDFYRNGLTDRDITVALSGSHSGKHAHPRSRSGDGAWTDP  180
    ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||

QY  181  LKFDNSYFLETLKGSSEGLKLPDALKLLDDEPFRRYVELYAKDDEVFKEKYDAESHKRLS  240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  181  LKFDNSYFLETLKGSSEGLKLPDALKLLDDEPFRRYVELYAKDDEVFKEKYDAESHKRLS  240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  241  ELGFPFRSSGPASTSDYSTAVVLAQSAVGAVAAYVYIAGLYEASRKS  291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  241  ELGFPFRSSGPASTSDYSTAVVLAQSAVGAVAAYVYIAGLYEASRKS  291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
S71279
L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis thaliana
```

N:Alternate names: protein M4E13.60
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: S71279; T05770
R:Jespersen, H.M.; Kjrsgaard, I.V.H.; Wejlander, K.G.
submitted to the EMBL Data Library, May 1996
A:Description: Ascorbate peroxidase isoenzymes in *Arabidopsis thaliana*.
A:Reference number: S71279
A:Accession: S71279
A:Molecule type: mRNA
A:Residues: 1-287 <JES>
A:Cross-references: EMBL:X98003; NID:91332438; PID:91332439
R:Bevan, M.; Punnelle, B.; Boutry, M.; Goffeau, A.; Hohsels, J.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15451
A:Accession: T05770
A:Molecule type: DNA
A:Residues: 1-287 <BEV>
A:Cross-references: EMBL:AL022023
A:Experimental source: cultivar Columbia; BAC clone M4E13
C:Genetics:
A:Gene: APX
A:Map position: 4
A:Introns: 38/2; 80/1; 96/3; 118/3; 135/1; 162/3; 189/2; 223/3
A:Note: M4E13.60
C:Superfamily: cytochrome-c peroxidase
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:40/Active site: His (distal axial ligand) #status predicted
F:160/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:116,205/Active site: Tyr, Asp #status predicted

Query Match	Similarity	79.0%	Score 1183	DB 2:	Length 287
Best Local	Similarity 75.9%		Pred. No. 1.7e-90		
Matches 221	Conservative 34		Mismatches 32	Indels 4	Gaps 1
QY	1	MAAPVADAEYLQVDRARRARFALIAASKCAIMLRLAHMDGTYDVNRTGANGSIRY	60		
		: ::: : : : : : : : : : :			
Db	1	MAAPVYDAEYLKETIKARRELRLSLANKKCAIMLRLANHMDGTYDAQSKTGGPNSTIN	60		
QY	61	BEEYTHGSNAGIKIALLDLEPIKAKHPKITTYADLQIAGVAAVEYGTPTVEITPGRDS	120		
		: : : : : : : : : : : : :			
Db	61	EEETHHGANSGLIKIALDCEGVKAKHPKITTYADVLQIAGVAAVEYTGPDYIFVPERKMS	120		
QY	121	SVCPREGRLPDAAKKCAPIHRIIDFYRMGLTDKRIVALSGHSISGAKHPEKSGPDGAATRP	180		
		: : : : : : : : : : : : :			
Db	121	NVCPREGRLPDAAKQGFQHIHRLDVEFYRMGLSDKDIVALSGCHTIGRAHPEKSGEDGPTWQRP	180		
QY	181	LKFDSYFLELLKGSEGLIKLPTDKALLDDPEFRFYVELYAKDEVEYFKQDAESHKKS	240		
		: : : : : : : : : : : : :			
Db	181	LKFDSYFVELLKGSEGLIKLPTDKTLLDEDFRFLVELYAKDKDEAFPRDYAESHKKS	240		
QY	241	ELGFNPRSGPASTKSDYSTAVVLIQSAAGVAAAVYAGVLYEAKSRSK	291		
		: : : : : : : : : : : : :			
Db	241	ELGFNPNSSAGKA---VADSTILLQSAAGVAAAVAAVAGFYETELRKKRK	287		

RESULT 3
T04707
L-ascorbate peroxidase (EC 1.11.1.11) T19K4.100 - Arabidopsis thaliana
N:Alternate names: protein F4B14.240
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #ssequence_revision 11-Jun-1999 #text_change 20-Apr-2000
C:Accession: T04707, T05489
R:Bevan, M.; Rose, M.; Hempel, S.; Ertlan, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, October 1998
A:Reference number: Z15380
A:Accession: T04707
A:Molecule type: DNA
A:Residues: 1-279 <EMBL>
A:Cross-references: EMBL:AL031986
A:Experimental source: cultivar Columbia; BAC clone F4B14
R:Bevan, M.; Weiler, H.; Wambutt, R.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.; Schellle
submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15418
A:Accession: T05489
A:Molecule type: DNA
A:Residues: 1-279 <BBN>
A:Cross-references: EMBL:AL022373
A:Experimental source: cultivar Columbia; BAC clone T19K4
C:Genetics:
A:Map position: 4
A:Introns: 37/2: 79/1; 95/3: 117/3; 133/1; 160/3; 187/2; 221/3
A:Note: FAP14.240: T19K4.100
C:Superfamily: cytochrome-c peroxidase
C:Keywords: heme; iron; metalloprotein; oxidoreductase
E:35/Active site: His (distal axial ligand) #status predicted
E:158/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:174,203/Active site: Trp, Asp #status predicted

Query Match 62.4%: Score 934.5; DB 2; Length 279;
Best Local Similarity 62.6%: Pred. No. 6.5e-70;
Matches 179; Conservative 42; Mismatches 54; Indels 11; Gaps 2;

[illegible]

```

RESULT 4
T07056
L-ascorbate peroxidase (EC 1.11.1.11) 2 - soybean
C|Species: Glycine max (soybean)
C|Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 19-May-2000
C|Accession: T07056
R|Turano, F.J.; McMahon, M.B.; Caldwell, C.R.
submitted to the EMBL Data Library, April 1996
A|Reference number: Z15888
A|Accession: T07056
A|Status: translated from GB/EMBL/DDBJ
A|Molecule type: mRNA
A|Residues: 1250 <TUR>
A|Cross-references: EMBL:U56634; NID:g1336081; PIDN:AAB01221.1; PTD:g1336082
A|Experimental source: cv. Century
C|Genetics:
A|Gene: APx2
C|Function:
A|Description: catalyzes peroxidation of ascorbate to dehydroascorbate
C|Superfamily: cytochrome-c peroxidase
C|Keywords: Chromoprotein; heme; Iron; metalloprotein; oxidoreductase
F|Active site: His (distal axial ligand) #status predicted
F|Binding site: heme iron (His) (proximal axial ligand) #status predicted
F|Other Active site: Trp, Asp #status predicted

Query Match          55.7%   Score 834.5; DB 2; Length 250;
Best local similarity 65.3%; Pred. No. 1.le-6l;
Matches 158; Conservative 32; Mismatches 51; Indels 1; Gaps 1;.

      4 PYVDATELRYDVARARAFRALIASKGCAPIMLRLAMHAGTYDVNTGTGCANSGIRYEER 63
      |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
db     6 PTYSADQKAEVFAKKRIKLGGFLTAERCAPLMILRLAMHSAGYDDVSSTGGPFGTIKHPSF 65

```


Query Match 55.0%; Score 824; DB 2; Length 249;
Best Local Similarity 64.3%; Pred. No. 8.1e-61;
Matches 155; Conservative 32; Mismatches 54; Indels 0; Gaps 0;

QY 4 PYYDAEYLROVRRARRAFALITASKCAPIMLRAMHAGTYDVNTRTGANGSIRYEE 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 6 PYYSEYQAIERAKKRLGLTAERKQCAPMLRLAMHSGTFCDSKGTGPFETMRKSE 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 64 YTHGSNAGLKIAIDLEPIKAKHPKITTYADLHQLAGVAVVETGPTVEFIPGRDSSVC 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 66 LAHGANGGLDIIVRLLEPIKEQFPITSYADFYQLAGVAVVETGPDVPHRGREDKPEP 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 124 PREGRLPDATKGSDDLROVFGAOMGLSDODIYALSGGHTLGRCHKBRSGPBTMRPLQ 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 126 PREGRLPDATKGSDDLROVFGAOMGLSDODIYALSGGHTLGRCHKBRSGPBTMRPLQ 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 184 DMSYFLELLKGSEGLIKLPDTRKALLDDPEFRRYVELYAKDEVFYKDESHKKTSEL 243
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 186 DMSYFLELLKGSEGLIKLPDTRKALLDDPEFRRYVELYAKDEVFYKDESHKKTSEL 243
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 244 F 244
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 246 F 246

RESULT 8

T09125
L-ascorbate peroxidase (EC 1.11.1.11) [validated] - rice
N:Alternate names: 27K protein 4302; acetolactate synthetase I [misidentification]
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
A:Accession: T09125; PS0211; PA0113; PQ0736
R:Morita, S.; Kamihata, H.; Yokoi, H.; Masumura, T.; Tanaka, K.
A:Description: Cloning and characterization of a rice ascorbate peroxidase cDNA.
A:Reference number: 214968
A:Accession: T09125

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-250 <MOR>
A:Cross-references: EMBL:D45423
R:Tsuigita, A.; Kamo, M.
submitted to JIPID, April 1993
A:Reference number: PS0209
A:Accession: PS0211
A:Molecule type: protein
A:Residues: 2-17, 'X', 19 <TSU>
A:Experimental source: seed and callus (strain Nihonbare)
A:Note: molecular weight 27K, pI 5.5
R:Kamo, M.; Tsuigita, A.
submitted to JIPID, March 1995
A:Reference number: PA0114
A:Accession: PA0113
A:Molecule type: protein
A:Residues: 2-17, 'X', 19 <KAM>
A:Experimental source: seedling and callus
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: PQ0696
A:Accession: PQ0736
A:Status: preliminary
A:Molecule type: protein
A:Residues: 2, 'L', 4-19 <KOM>
C:Superfamily: cytochrome-c peroxidase
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:42/Active site: His (distal axial ligand) #status predicted
F:163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:179,208/Active site: Trp, Asp #status predicted

Query Match 54.8%; Score 821.5; DB 2; Length 250;
Best Local Similarity 64.5%; Pred. No. 1.3e-60;

Matches 156; Conservative 34; Mismatches 51; Indels 1; Gaps 1;

QY 4 PYYDAEYLROVRRARRAFALITASKCAPIMLRAMHAGTYDVNTRTGANGSIRYEE 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 6 PYYSAEYQAEVAKRQKRLALIAEKSCAPMLRLAMHSGTIDVSKGTGPGTKTAE 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 64 YTHGSNAGLKIAIDLEPIKAKHPKITTYADLHQLAGVAVVETGPTVEFIPGRDSSVC 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 66 LSHANAGGLDIIVRLLEPIKEQFPITSYADFYQLAGVAVVETGPDVPHRGREDKPEP 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 124 PREGRLPDATKGSDDLROVFGAOMGLSDODIYALSGGHTLGRCHKBRSGPBTMRPLQ 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 126 PREGRLPDATKGSDDLROVFGAOMGLSDODIYALSGGHTLGRCHKBRSGPBTMRPLQ 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 183 FDNYSFLELLKGSEGLIKLPDTRKALLDDPEFRRYVELYAKDEVFYKDESHKKTSEL 242
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 186 FDNYSFLELLKGSEGLIKLPDTRKALLDDPEFRRYVELYAKDEVFYKDESHKKTSEL 242
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 243 GF 244
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 246 GF 247

RESULT 9

T09125
L-ascorbate peroxidase (EC 1.11.1.11) - spinach
C:Species: Spinacia oleracea (spinach)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
A:Accession: T09125
R:Webb, R.P.; Allen, R.D.
Plant Physiol. 108, 1325, 1995
A:Title: Isolation and characterization of a cDNA for spinach cytosolic ascorbate per
A:Reference number: 216576; MUID:95357433
A:Accession: T09125
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-250 <WEB>
A:Cross-references: EMBL:L20864; NID:g310586; PIDN:AAA9518.1; PID:g310587
A:Experimental source: leaf
C:Function:
A:Description: catalyzes peroxidation of ascorbate to dehydroascorbate
C:Superfamily: cytochrome-c peroxidase
C:Keywords: chromoprotein; cytosol; heme; iron; metalloprotein; oxidoreductase
F:42/Active site: His (distal axial ligand) #status predicted
F:163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:179,208/Active site: Trp, Asp #status predicted

Query Match 54.7%; Score 819.5; DB 2; Length 250;
Best Local Similarity 64.0%; Pred. No. 1.9e-60;
Matches 155; Conservative 31; Mismatches 55; Indels 1; Gaps 1;

QY 4 PYYDAEYLROVRRARRAFALITASKCAPIMLRAMHAGTYDVNTRTGANGSIRYEE 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 6 PYYSEYQAIERAKKRLGLTAERKQCAPMLRLAMHSGTFCDSKGTGPFETMRKSE 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 64 YTHGSNAGLKIAIDLEPIKAKHPKITTYADLHQLAGVAVVETGPTVEFIPGRDSSVC 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 66 LAHGANGGLDIIVRLLEPIKEQFPITSYADFYQLAGVAVVETGPDVPHRGREDKPEP 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 124 PREGRLPDATKGSDDLROVFGAOMGLSDODIYALSGGHTLGRCHKBRSGPBTMRPLQ 182
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 126 PREGRLPDATKGSDDLROVFGAOMGLSDODIYALSGGHTLGRCHKBRSGPBTMRPLQ 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 183 FDNYSFLELLKGSEGLIKLPDTRKALLDDPEFRRYVELYAKDEVFYKDESHKKTSEL 242
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 186 FDNYSFLELLKGSEGLIKLPDTRKALLDDPEFRRYVELYAKDEVFYKDESHKKTSEL 242
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 243 GF 244
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
Db 246 GF 247

RESULT 10

